SEQUENCE LISTING

<110> Odyssey Thera, Inc.

Michnick, Stephen MacDonald, Marnie Lamerdin, Jane <120> FRAGMENTS OF FLUORESCENT PROTEINS FOR PROTEIN-FRAGMENT COMPLEMENTATION ASSAYS <130> ODDY007 <150> US 60/461,133 <151> 2003-04-09 <160> 1067 <170> PatentIn version 3.0 <210> 1 <211> 714 <212> DNA <213> Aequorea victoria <220> <221> CDS <222> (1)..(714) <223> wild-type green fluorescent protein <400> 1 atg agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca att ctt gtt 48 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc 144 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys act act gga aaa cta cct gtt cca tgg cca aca ctt gtc act act ttc 192 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe

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cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

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Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

105

100

240

288

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		aaa Lys														432
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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
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Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

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<302> Creating new fluorescent probes for cell biology

<303> Nat. Rev. Mol. Cell Biol.

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Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
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Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
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                                105
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
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Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
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Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
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Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
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Pro Val Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
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165

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Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
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Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
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Phe Asn Tyr Gly Asn Arg Val Phe Thr Glu Tyr Pro Gln Asp Ile Val 65 70 75 80

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Phe Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Ala Asp Ile Thr

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Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Asp Asn

130 135 140

Trp Glu Pro Ser Cys Glu Lys Ile Ile Pro Val Pro Lys Gln Gly Ile 150 155 Leu Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Leu Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Arg 185 Lys Met Pro Asp Trp His Phe Ile Gln His Lys Leu Thr Arg Glu Asp 200 Arg Ser Asp Ala Lys Asn Gln Lys Trp His Leu Thr Glu His Ala Ile Ala Ser Gly Ser Ala Leu Pro <210> 10 <211> 231 <212> PRT <213> Anthozoa zoanthus; <220> <221> misc feature <223> Zoanthus ("z") FP538 <300> <301> Matz, M.V. et al <302> Fluorescent proteins from nonbioluminescent Anthozoa species <303> Nat. Biotech. <304> 17 <305> 10 969-73 <306> <307> 1999-<313> (1)..(231) <400> 10 Met Ala His Ser Lys His Gly Leu Lys Glu Glu Met Thr Met Lys Tyr 5 15 His Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr Gly Glu Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn Leu Cys Val 35 40 Ile Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Gly Phe Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr Pro Gln Asp Ile Val Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gly Arg Ser 90

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Val Ser Val Lys Glu Asn Cys Ile Tyr His Lys Ser Ile Phe Asn Gly Met Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr Asn 135 Trp Glu Ala Ser Cys Glu Lys Ile Met Pro Val Pro Lys Gln Gly Ile Leu Lys Gly Asp Val Ser Met Tyr Leu Leu Lys Asp Gly Gly Arg Tyr Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Ser 185 Lys Met Pro Glu Trp His Phe Ile Gln His Lys Leu Leu Arg Glu Asp 195 200 Arg Ser Asp Ala Lys Asn Gln Lys Trp Gln Leu Thr Glu His Ala Ile 215 220 Ala Phe Pro Ser Ala Leu Ala 225 230 <210> 11 <211> 232 <212> PRT <213> Anthozoa discosoma; <220> <221> misc_feature <223> Discosoma striata ("ds") FP483 <300> <301> Matz, M.V. et al <302> Fluorescent proteins from nonbioluminescent Anthozoa species <303> Nat. Biotech. <304> 17 <305> 10 <306> 969-73 <307> 1999-<313> (1)..(232) <400> 11 Met Ser Cys Ser Lys Ser Val Ile Lys Glu Glu Met Leu Ile Asp Leu His Leu Glu Gly Thr Phe Asn Gly His Tyr Phe Phe Ile Lys Gly Lys Gly Lys Gly Gln Pro Asn Glu Gly Thr Asn Thr Val Thr Leu Glu Val Thr Lys Gly Gly Pro Leu Pro Phe Gly Trp His Ile Leu Cys Pro Gln

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Asp Tyr Leu Lys Leu Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser
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Ser Asn Ala Phe Gln Tyr Gly Asn Arg Ala Leu Thr Lys Tyr Pro Asp

Asp Ile Ala Asp Tyr Phe Lys Gln Ser Phe Pro Glu Gly Tyr Ser Trp

Glu Arg Thr Met Thr Phe Glu Asp Lys Gly Ile Val Lys Val Lys Ser

Asp Ile Ser Met Glu Glu Asp Ser Phe Ile Tyr Glu Ile Arg Phe Asp 120

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Lys Trp Glu Pro Ser Thr Glu Ile Met Tyr Val Arg Asp Gly Val Leu 150

Val Gly Asp Ile Ser His Ser Leu Leu Glu Gly Gly Gly His Tyr

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Asp Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
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Ile Lys Met Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu
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Arg	Met	Glu	Gly 20	Ser	Val	Asn	Gly	His 25	Glu	Phe	Glu	Ile	Glu 30	Gly	Glu	
Gly	Glu	Gly 35	Arg	Pro	Tyr	Glu	Gly 40	Thr	Gln	Thr	Ala	Lys 45	Leu	Lys	Val	
Thr	Lys 50	Gly	Gly	Pro	Leu	Pro 55	Phe	Ala	Trp	Asp	Ile 60	Leu	Ser	Pro	Gln	
Phe 65	Gln	Tyr	Gly	Ser	Lys 70	Ala	Tyr	Val	Lys	His 75	Pro	Ala	Asp	Ile	Pro 80	
Asp	Tyr	Leu	Lys	Leu 85	Ser	Phe	Pro	Glu	Gly 90	Phe	Lys	Trp	Glu	Arg 95	Val	
Met	Asn	Phe	Gl <u>u</u> 100	Asp	Gly	Gly	Val	Val 105	Thr		Thr	Gln	Asp 110	Ser	Ser	
Leu	Gln	Asp 115	Gly	Glu	Phe	Ile	Tyr 120	Lys	Val	Lys	Leu	Arg 125	Gly	Thr	Asn	
Phe	Pro 130	Ser	Asp	Gly	Pro	Val 135	Met	Gln	Lys	Lys	Thr 140	Met	Gly	Trp	Glu	

145	Thr Gli	a Arg	Met 150	Tyr	Pro	Glu	Asp	Gly 155	Ala	Leu	Lys	Gly	Glu 160		
Ile Lys	Met Arg	Leu 165	Lys	Leu	Lys	Asp	Gly 170	Gly	His	Tyr	Asp	Ala 175	Glu		
Val Lys	Thr Thi		Met	Ala	Lys	Lys 185	Pro	Val	Gln	Leu	Pro 190	Gly	Ala		
Tyr Lys	Thr Asg 195	lle	Lys	Leu	Asp 200	Ile	Thr	Ser	His	Asn 205	Glu	Asp	Tyr		
Thr Ile	Val Glı	Gln	Tyr	Glu 215	Arg	Ala	Glu	Gly	Arg 220	His	Ser	Thr	Gly		
Ala 225															
<211> 6 <212> D	7 96 NA rtifici	al													
	KFP1" a		ated	vari	iant	of A	cind]	ling	fluc	oreso	cent	prot	cein	asCP f	Ēro
<223> " m < <220> <221> C		cata	ated	vari	iant	of }	kindl	ling	fluc	oreso	cent	prot	cein	asCP f	Ēro
<223> " m < <220> <221> C	DS 1)(69 7 tcc ctg	cata 6)	acc	gag	acc	atg	ccc	ttc	aag	acc	acc	atc	gag	asCP f	Ero
<223> "	DS 1)(69 7 tcc ctc Ser Let	cata 6) ctg Leu 5	acc Thr	gag Glu tgc	acc Thr	atg Met aag	ccc Pro 10	ttc Phe	aag Lys ggc	acc Thr	acc Thr	atc Ile 15	gag Glu ggc	asCP f	
<223> " <220> <221> C <222> (<400> 1 atg gcc Met Ala 1 ggc acc Gly Thr aac ccc Asn Pro	TA. sul	cata 6) ctg Leu 5	acc Thr cac His	gag Glu tgc Cys cag	acc Thr ttc Phe	atg Met aag Lys 25	ccc Pro 10 tgc Cys	ttc Phe atc Ile	aag Lys ggc Gly	acc Thr aag Lys	acc Thr ggc Gly 30 atc	atc Ile 15 gag Glu	gag Glu ggc Gly		48
<223> " <220> <221> C <222> (<400> 1 atg gcc Met Ala 1 ggc acc Gly Thr aac ccc Asn Pro	TA. sul	cata 6) ctg Leu 5 ggc Gly ggc Gly	acc Thr cac His acc Thr	gag Glu tgc Cys cag Gln	acc Thr ttc Phe gag Glu 40 cac	atg Met aag Lys 25 atg Met	ccc Pro 10 tgc Cys aag Lys	ttc Phe atc Ile atc	aag Lys ggc Gly gag Glu acc	acc Thr aag Lys gtg Val 45 tcc	acc Thr ggc Gly 30 atc Ile	atc Ile 15 gag Glu gag Glu	gag Glu ggc Gly ggc Gly	1	48

aag Lys	cag Gln	tcc Ser	ttc Phe	ccc Pro 85	gag Glu	ggc Gly	ttc Phe	acc Thr	tgg Trp 90	gag Glu	cgc Arg	acc Thr	acc Thr	acc Thr 95	tac Tyr		288
	gac Asp																336
	tgc Cys																384
	ggc Gly 130																432
	atc Ile																480
	ctg Leu																528
	tac Tyr																576
	ttc Phe																624
	tgc Cys 210																672
	ccc Pro																696
<210 <211 <211 <211	2> I	232 PRT	icia	al													
<220 <220	3> '		l" a sulo		ated	vari	lant	of }	cind]	ling	fluc	oreso	cent	prot	ein	asCP	fro
<400	0> 1	18															
Met 1	Ala	Ser	Leu	Leu 5	Thr	Glu	Thr	Met	Pro 10	Phe	Lys	Thr	Thr	Ile 15	Glu		
Gly	Thr	Val	Asn 20	Gly	His	Cys	Phe	Lys 25	Cys	Ile	Gly	Lys	Gly 30	Glu	Gly		

Asn Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly 35 40 45

Gly Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr 50 60

Gly Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe 65 70 75 80

Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Tyr 85 90 95

Glu Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly 100 105 110

Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala 115 120 125

Asp Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr 130 140

Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met 145 150 155 160

Ala Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr 165 170 175

Thr Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe
180 185 190

His Phe Glu Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys Gly
195 200 205

Lys Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala 210 215 220

Ala Pro Ser Lys Leu Gly His Asn 225 230

<210> 19

<211> 10

<212> PRT

<213> Artificial

<220>

<223> flexible linker

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<400> 19
Gly Gly Gly Ser Gly Gly Gly Ser
               5
<210> 20
<211> 114
<212> DNA
<213> Artificial
<220>
<223> modified fragment= GFP F1(aa 1-39 of wt GFP) w/o. Met @ position
1
<220>
<221> CDS
<222>
      (1)..(114)
<400> 20
agt aaa gga gaa ctt ttc act gga gtt gtc cca att ctt gtt gaa
                                                                     48
Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
               5
tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag ggt
                                                                     96
Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
                               25
gaa ggt gat gca aca tac
                                                                    114
Glu Gly Asp Ala Thr Tyr
       35
<210> 21
<211> 38
<212> PRT
<213> Artificial
220>
<223> modified fragment= GFP F1 (aa 1-39 of wt GFP) w/o. Met @ position
<400> 21
Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
           20
                               25
Glu Gly Asp Ala Thr Tyr
       35
<210> 22
<211> 600
<212> DNA
<213> Artificial
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modified frag.; GFP F2 (aa 40-238 of wt GFP) + Met @ position 1 <223> <220> <221> CDS <222> (1)...(600)<400> 22 atg gga aaa ctt acc ctt aaa ttt att tgc act act gga aaa cta cct 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtt cca tgg cca aca ctt gtc act act ttc tct tat ggt gtt caa tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys 25 144 ttt tca aga tac cca gat cat atg aaa cgg cat gac ttt ttc aag agt Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 40 gcc atg ccc gaa ggt tat gta cag gaa aga act ata ttt ttc aaa gat 192 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp gac ggg aac tac aag aca cgt gct gaa gtc aag ttt gaa ggt gat acc 240 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr ctt gtt aat aga atc gag tta aaa ggt att gat ttt aaa gaa gat gga 288 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 aac att ctt gga cac aaa ttg gaa tac aac tat aac tca cac aat gta 336 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 tac atc atg gca gac aaa caa aag aat gga atc aaa gtt aac ttc aaa 384 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 att aga cac aac att gaa gat gga agc gtt caa cta gca gac cat tat 432 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 480 caa caa aat act cca att ggc gat ggc cct gtc ctt tta cca gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 cat tac ctg tcc aca caa tct gcc ctt tcg aaa gat ccc aac gaa aag 528 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 aga gac cac atg gtc ctt ctt gag ttt gta aca gct gct ggg att aca 576 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 600 cat ggc atg gat gaa cta tac aaa His Gly Met Asp Glu Leu Tyr Lys

<211> 200 <212> PRT <213> Artificial <220> <223> modified frag.; GFP F2 (aa 40-238 of wt GFP) + Met @ position 1 <400> 23 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys 25 Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 40 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 150 145 155 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185

<210> 23

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<210> 24
<211> 117
<212> DNA
<213> Artificial
<220>
<223>
      modified frag.; YFP F1A (aa 1-40 of EYFP) - Met @ position 1
<220>
<221>
      CDS
<222> (1)..(117)
<400> 24
gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg gtc
                                                                      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                5
                                    10
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
                                                                      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
                                25
ggc gag ggc gat gcc acc tac
                                                                     117
Gly Glu Gly Asp Ala Thr Tyr
        35
<210> 25
<211> 39
<212> PRT
<213> Artificial
<220>
<223> modified frag.; YFP F1A (aa 1-40 of EYFP) - Met @ position 1
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                5
                                    10
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20
                                25
Gly Glu Gly Asp Ala Thr Tyr
        35
<210> 26
<211>
       600
<212>
      DNA
<213>
      Artificial
<220>
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His Gly Met Asp Glu Leu Tyr Lys

<223> modified frag.; YFP F2A (aa 41-239 of EYFP) + Met @ position 1

<22 <22 <22	1>	CDS (1):	. (60	0)												
	ggc	26 aag Lys														48
		tgg Trp														96
		cgc Arg 35														144
		ccc Pro														192
gac Asp 65	ggc Gly	aac Asn	tac Tyr	aag Lys	acc Thr 70	cgc Arg	gcc Ala	gag Glu	gtg Val	aag Lys 75	ttc Phe	gag Glu	ggc Gly	gac Asp	acc Thr 80	240
		aac Asn														288
		ctg Leu														336
tat Tyr	atc	atg Met 115	gcc Ala	gac Asp	aag Lys	cag Gln	aag Lys 120	aac Asn	ggc Gly	atc Ile	aag Lys	gtg Val 125	aac Asn	ttc Phe	aag Lys	384
atc Ile	cgc Arg 130	cac His	aac Asn	atc Ile	gag Glu	gac Asp 135	ggc Gly	agc Ser	gtg Val	cag Gln	ctc Leu 140	gcc Ala	gac Asp	cac His	tac Tyr	432
		aac Asn														480
		ctg Leu														528
		cac His														576
		atg Met 195														600

<210> 27

<211> 200

<212> PRT

<213> Artificial

<220>

<223> modified frag.; YFP F2A (aa 41-239 of EYFP) + Met @ position 1

<400> 27

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys 195 200

```
<210>
       28
<211>
       597
<212>
       DNA
<213>
       Artificial
<220>
<223>
       modified frag.; YFPF2A w. F46L mutation
<220>
<221>
       CDS
<222>
       (1)..(597)
<400> 28
ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc gtg
                                                                        48
Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val
ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc
                                                                       144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
                             40
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac
                                                                       192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50
                        55
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg
                                                                       240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac
                                                                       288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat
                                                                      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100
                                 105
atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc
                                                                       384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115
                                                 125
ege cae aac ate gag gae gge age gtg cag ete gee gae cae tae cag
                                                                       432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130
                        135
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac
                                                                       480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145
                    150
                                         155
                                                             160
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc
                                                                      528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165
                                     170
                                                         175
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc
                                                                      576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
```

597

ggc atg gac gag ctg tac aag Gly Met Asp Glu Leu Tyr Lys

195

<210> 29

<211> 199

<212> PRT <213> Artificial

<220>

<223> modified frag.; YFPF2A w. F46L mutation

<400> 29

Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 25 20

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 70

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 170

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 $$ 185 $$ 190 $$

Gly Met Asp Glu Leu Tyr Lys 195

<210> 30 <211> 600 <212> DNA <213> Artificial
<220> <223> modified frag., YFPF2A w. F46L mutation + Met @ postion 1
<220> <221> CDS <222> (1)(600)
<pre><400> 30 atg ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro 1</pre>
gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 25 30
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn

145	150	155	160
His Tyr Leu Ser		c ctg agc aaa gac ccc a Leu Ser Lys Asp Pro 170	
		g ttc gtg acc gcc gcc u Phe Val Thr Ala Ala 185	
ctc ggc atg gac g Leu Gly Met Asp (5	600
<210> 31 <211> 200 <212> PRT <213> Artificia	1		
<220> <223> modified f	frag., YFPF2A	w. F46L mutation +	Met @ postion 1
<400> 31	•		
	Thr Leu Lys Le 5	ı Ile Cys Thr Thr Gly 10	Lys Leu Pro 15
Val Pro Trp Pro 7	Thr Leu Val Th	r Thr Phe Gly Tyr Gly 25	Leu Gln Cys 30
Phe Ala Arg Tyr I	Pro Asp His Me 40	Lys Arg His Asp Phe 45	Phe Lys Ser
Ala Met Pro Glu (Gly Tyr Val Gla 55	n Glu Arg Thr Ile Phe 60	Phe Lys Asp
Asp Gly Asn Tyr I	Lys Thr Arg Ala	a Glu Val Lys Phe Glu 75	Gly Asp Thr 80
	Ile Glu Leu Ly: 35	s Gly Ile Asp Phe Lys 90	Glu Asp Gly 95
Asn Ile Leu Gly H	His Lys Leu Gl	ı Tyr Asn Tyr Asn Ser 105	His Asn Val
Tyr Ile Met Ala A	Asp Lys Gln Ly: 12	s Asn Gly Ile Lys Val	_
Ile Arg His Asn I	Ile Glu Asp Gly 135	y Ser Val Gln Leu Ala 140	Asp His Tyr

Gln Gln Asn Thr Pro	o Ile Gly Asp Gl 150	Pro Val Leu Leu 155	Pro Asp Asn 160
His Tyr Leu Ser Tyr 165		Ser Lys Asp Pro 170	Asn Glu Lys 175
Arg Asp His Met Val	L Leu Leu Glu Ph 18		Gly Ile Thr 190
Leu Gly Met Asp Glu 195	ı Leu Tyr Lys 200		
<210> 32 <211> 597 <212> DNA <213> Artificial			
<220> <223> modified fra	ag.; YFPF2A wit	ı F46L/F64L mutat	cions
<220> <221> CDS <222> (1)(597)	·		
<400> 32 ggc aag ctg acc ctg Gly Lys Leu Thr Leu 1 5			
ccc tgg ccc acc ctc Pro Trp Pro Thr Let 20			
gcc cgc tac ccc gad Ala Arg Tyr Pro Asp 35			
atg ccc gaa ggc tad Met Pro Glu Gly Tyn 50			
ggc aac tac aag acc Gly Asn Tyr Lys Thi 65	c cgc gcc gag gt Arg Ala Glu Va 70	g aag ttc gag ggc . Lys Phe Glu Gly 75	gac acc ctg 240 Asp Thr Leu 80
gtg aac cgc atc gag Val Asn Arg Ile Glu 85			
atc ctg ggg cac aag Ile Leu Gly His Lys 100		Tyr Asn Ser His	

	12	20	125
		gc gtg cag ctc gcc er Val Gln Leu Ala 140	
		gc ccc gtg ctg ctg ly Pro Val Leu Leu 155	
		tg agc aaa gac ccc eu Ser Lys Asp Pro 170	
		tc gtg acc gcc gcc he Val Thr Ala Ala 185	
ggc atg gac gag Gly Met Asp Glu 195			597
<210> 33 <211> 199 <212> PRT <213> Artificia	al		
<220> <223> modified	frag.; YFPF2A	with F46L/F64L m	nutations
<400> 33			
Gly Lys Leu Thr 1	Leu Lys Leu II 5	le Cys Thr Thr Gly 10	Lys Leu Pro Val 15
1	5		15
Pro Trp Pro Thr 20	5 Leu Val Thr Th	hr Leu Gly Tyr Gly 25 ys Arg His Asp Phe	15 Leu Gln Cys Phe 30
Pro Trp Pro Thr 20 Ala Arg Tyr Pro 35	Leu Val Thr Th Asp His Met Ly	hr Leu Gly Tyr Gly 25 ys Arg His Asp Phe	Leu Gln Cys Phe 30 Phe Lys Ser Ala
Pro Trp Pro Thr 20 Ala Arg Tyr Pro 35 Met Pro Glu Gly 50	Leu Val Thr Th Asp His Met Ly 40 Tyr Val Gln G	hr Leu Gly Tyr Gly 25 ys Arg His Asp Phe 0 lu Arg Thr Ile Phe	Leu Gln Cys Phe 30 Phe Lys Ser Ala 45 Phe Lys Asp Asp
Pro Trp Pro Thr 20 Ala Arg Tyr Pro 35 Met Pro Glu Gly 50 Gly Asn Tyr Lys 65	Leu Val Thr The Asp His Met Ly 40 Tyr Val Gln Gi 55 Thr Arg Ala Gi 70	hr Leu Gly Tyr Gly 25 ys Arg His Asp Phe 0 lu Arg Thr Ile Phe 60 lu Val Lys Phe Glu	Leu Gln Cys Phe 30 Phe Lys Ser Ala 45 Phe Lys Asp Asp Gly Asp Thr Leu 80

Ile Met Ala 115	Asp Lys Gl	n Lys Asr 120	_	_	Asn Phe 125	Lys Ile	
Arg His Asn 130	Ile Glu Asp	o Gly Ser 135	Val Gln	Leu Ala	Asp His	Tyr Gln	
Gln Asn Thr 145	Pro Ile Gl		Pro Val	Leu Leu 155	Pro Asp	Asn His 160	
Tyr Leu Ser	Tyr Gln Se: 165	r Ala Leu	Ser Lys 170		Asn Glu	Lys Arg 175	
Asp His Met	Val Leu Len 180	ı Glu Phe	Val Thr	Ala Ala	Gly Ile 190	Thr Leu	
Gly Met Asp 195	Glu Leu Ty:	c Lys					
<210> 34 <211> 600 <212> DNA <213> Artif	icial						•
<220> <223> modif	ied frag.;	YFPF2A	w. F46L	/F64L mu	tations	+ Met @	posit. 1
		YFPF2A	w. F46L	/F64L mu	tations	+ Met @	posit. 1
<223> modif <220> <221> CDS	(600)	g aag ctg	atc tgc	acc acc	ggc aag	ctg ccc	posit. 1
<223> modifications and the control of the control	(600) ctg acc ctc Leu Thr Let 5 ccc acc ctc	g aag cto 1 Lys Leu 2 gtg acc	atc tgc Ile Cys 10	acc acc Thr Thr	ggc aag Gly Lys ggc ctg	ctg ccc Leu Pro 15 cag tgc	
<223> modifications and the control of the control	ctg acc ctc Leu Thr Lei 5 ccc acc ctc Pro Thr Lei 20	g aag ctg 1 Lys Leu c gtg acc 1 Val Thr	atc tgc lle Cys 10 acc ctg Thr Leu 25	acc acc Thr Thr ggc tac Gly Tyr cac gac His Asp	ggc aag Gly Lys ggc ctg Gly Leu 30 ttc ttc	ctg ccc Leu Pro 15 cag tgc Gln Cys	48
<223> modifications and the control of the control	ctg acc ctc Leu Thr Lei 5 ccc acc ctc Pro Thr Lei 20 tac ccc gac Tyr Pro Asj	g aag ctg Lys Leu c gtg acc l Val Thr c cac atg His Met 40	atc tgc Ile Cys 10 acc ctg Thr Leu 25 aag cgg Lys Arg	acc acc Thr Thr ggc tac Gly Tyr cac gac His Asp	ggc aag Gly Lys ggc ctg Gly Leu 30 ttc ttc Phe Phe 45	ctg ccc Leu Pro 15 cag tgc Gln Cys aag tcc Lys Ser	48
<223> modifications and the control of the control	ctg acc ctg Leu Thr Lei 5 ccc acc ctg Pro Thr Lei 20 tac ccc gaa Tyr Pro As gaa ggc taa Glu Gly Ty: tac aag acc	g aag ctg Lys Led c gtg acc l Val Thr c cac atg His Met 40 c gtc cag val Glr 55	atc tgc Ile Cys 10 acc ctg Thr Leu 25 aag cgg Lys Arg gag cgc	acc acc Thr Thr ggc tac Gly Tyr cac gac His Asp acc atc Thr Ile 60 aag ttc	ggc aag Gly Lys ggc ctg Gly Leu 30 ttc ttc Phe Phe 45 ttc ttc Phe Phe	ctg ccc Leu Pro 15 cag tgc Gln Cys aag tcc Lys Ser aag gac Lys Asp	48 96 144

		90	95
aac atc ctg ggg cac Asn Ile Leu Gly His 100			
tat atc atg gcc gac Tyr Ile Met Ala Asp 115			
atc cgc cac aac atc Ile Arg His Asn Ile 130			
cag cag aac acc ccc Gln Gln Asn Thr Pro 145			
cac tac ctg agc tac His Tyr Leu Ser Tyr 165			
cgc gat cac atg gtc Arg Asp His Met Val 180			
ctc ggc atg gac gag Leu Gly Met Asp Glu 195			600
<210> 35			
<211> 200 <212> PRT <213> Artificial			
<211> 200 <212> PRT <213> Artificial <220>	J.; YFPF2A w. F4	6L/F64L mutations	+ Met @ posit. 1
<211> 200 <212> PRT <213> Artificial <220>	g.; YFPF2A w. F4	.6L/F64L mutations	+ Met @ posit. 1
<pre><211> 200 <212> PRT <213> Artificial <220> <223> modified frag</pre>			_
<pre><211> 200 <212> PRT <213> Artificial <220> <223> modified frag <400> 35 Met Gly Lys Leu Thr</pre>	Leu Lys Leu Ile	Cys Thr Thr Gly Lys 10	Leu Pro 15
<pre><211> 200 <212> PRT <213> Artificial <220> <223> modified frag <400> 35 Met Gly Lys Leu Thr 1 5</pre> Val Pro Trp Pro Thr	Leu Lys Leu Ile Leu Val Thr Thr 25	Cys Thr Thr Gly Lys 10 Leu Gly Tyr Gly Leu 30	Leu Pro 15 Gln Cys
<pre><211> 200 <212> PRT <213> Artificial <220> <223> modified frag <400> 35 Met Gly Lys Leu Thr 1 5 Val Pro Trp Pro Thr 20 Phe Ala Arg Tyr Pro</pre>	Leu Lys Leu Ile Leu Val Thr Thr 25 Asp His Met Lys 40	Cys Thr Thr Gly Lys 10 Leu Gly Tyr Gly Leu 30 Arg His Asp Phe Phe 45	Leu Pro 15 Gln Cys Lys Ser

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95	
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110	
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125	
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140	
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190	
Leu Gly Met Asp Glu Leu Tyr Lys 195 200	
<210> 36 <211> 597 <212> DNA <213> Artificial	
<220> <223> modified frag.; YFPF2A with F64L mutation	
<220> <221> CDS <222> (1)(597)	
<pre><400> 36 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 1 5 10 15</pre>	18
ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc ttc Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe 20 25 30	96
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45	14
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac)2

Met	Pro 50	Glu	Gly	Tyr	Val	Gln 55	Glu	Àrg	Thr	Ile	Phe 60	Phe	Lys	Asp	Asp	·
ggc Gly 65	aac Asn	tac Tyr	aag Lys	acc Thr	cgc Arg 70	gcc Ala	gag Glu	gtg Val	aag Lys	ttc Phe 75	gag Glu	ggc Gly	gac Asp	acc Thr	ctg Leu 80	240
	aac Asn															288
	ctg Leu															336
	atg Met															384
	cac His 130															432
	aac Asn															480
	ctg Leu															528
	cac His														ctc Leu	576
	atg Met							٠								597
<210 <210 <210 <210	1> : 2> :	37 199 PRT Artii	ficia	al												
<22 <22		nodi	fied	frag	g.; Y	YFPF2	2 A v	vith	F64	1L որ	ıtat:	ion				
<40	0> 3	37														
Gly 1	Lys	Leu	Thr	Leu 5	Lys	Phe	Ile	Cys	Thr 10	Thr	Gly	Lys	Leu	Pro 15	Val	
Pro	Trp	Pro	Thr 20	Leu	Val	Thr	Thr	Leu 25	Gly	Tyr	Gly	Leu	Gln 30	Cys	Phe	
Ala	Arg	Tyr 35	Pro	Asp	His	Met	Lys 40	Arg	His	Asp	Phe	Phe 45	Lys	Ser	Ala	

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 105 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 135 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 150 155 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 38 <211> 600 <212> DNA <213> Artificial <220> <223> modified frag.; YFPF2A w. F64L mutation + Met @ position 1 <220> <221> CDS <222> (1)..(600) <400> 38 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc 96

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp

55

Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys 20 25 30

```
ttc gcc cgc tac ccc gac cac atq aaq cqq cac qac ttc ttc aaq tcc
                                                                     144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac
                                                                     192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc
                                                                      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                     288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
                                                                     336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100
                                105
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag
                                                                     384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115
ate ege cae aac ate gag gae gge age gtg cag ete gee gae cae tae
                                                                     432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
                        135
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac
                                                                     480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                    150
                                        155
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag
                                                                     528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165
                                    170
ege gat cae atg gte etg etg gag tte gtg ace gee geg gte act
                                                                     576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
           180
                                185
                                                    190
ctc ggc atg gac gag ctg tac aag
                                                                     600
Leu Gly Met Asp Glu Leu Tyr Lys
<210> 39
<211> 200
<212> PRT
<213> Artificial
<220>
<223> modified frag.; YFPF2A w. F64L mutation + Met @ position 1
<400> 39
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
                                    10
```

Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys 20 25 30.

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 · 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys 195 200

<210> 40

<211> 597

<212> DNA

<213> Artificial

<220>

<223> modified frag.; YFPF2A with K79R mutation

<220>

<221> CDS

<222> (1)..(597)

<400> 40 ggc aag ctg Gly Lys Leu 1	acc ctg aa Thr Leu Ly 5	g ttc atc s Phe Ile	tgc acc Cys Thr 10	acc ggc Thr Gly	aag ctg Lys Leu	ccc gtg Pro Val 15	48
ccc tgg ccc Pro Trp Pro							96
gcc cgc tac Ala Arg Tyr 35							144
atg ccc gaa Met Pro Glu 50							192
ggc aac tac Gly Asn Tyr 65	aag acc cg Lys Thr Ar 70	c gcc gag g Ala Glu	gtg aag Val Lys	ttc gag Phe Glu 75	ggc gac Gly Asp	acc ctg Thr Leu 80	240
gtg aac cgc Val Asn Arg	atc gag ct Ile Glu Le 85	g aag ggc 1 Lys Gly	atc gac Ile Asp 90	ttc aag Phe Lys	gag gac Glu Asp	ggc aac Gly Asn 95	288
atc ctg ggg Ile Leu Gly							336
atc atg gcc Ile Met Ala 115							384
cgc cac aac Arg His Asn 130							432
cag aac acc Gln Asn Thr 145	ccc atc gg Pro Ile Gl 15	Asp Gly	ccc gtg Pro Val	ctg ctg Leu Leu 155	ccc gac Pro Asp	aac cac Asn His 160	480
tac ctg agc Tyr Leu Ser	tac cag to Tyr Gln Se 165	gcc ctg Ala Leu	agc aaa Ser Lys 170	gac ccc Asp Pro	aac gag Asn Glu	aag cgc Lys Arg 175	528
gat cac atg Asp His Met	gtc ctg ctg Val Leu Le 180	g gag ttc ı Glu Phe	gtg acc Val Thr 185	gcc gcc Ala Ala	ggg atc Gly Ile 190	act ctc Thr Leu	576
ggc atg gac Gly Met Asp 195							597
<210> 41 <211> 199 <212> PRT <213> Artif	Eicial						

<220>

<223> modified frag.; YFPF2A with K79R mutation

<400> 41

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 30

Ala Arg Tyr Pro Asp His Met Arg Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

Gly Met Asp Glu Leu Tyr Lys 195

<210> 42

<211> 600

<212> DNA

<213>	Arti	ficia	al													
<220> <223>	modi	fied	fra	g.; :	YFPF	2 A v	with	K79	9R mι	ıtati	ion -	+ Met	: @ r	posit	. 1	
<220> <221> <222>	CDS	. (60	0)													
<400> atg gg Met Gl 1																48
gtg cc Val Pr																96
ttc gc Phe Al																144
gcc at Ala Me 50	t Pro															192
gac gg Asp Gl 65																240
ctg gt Leu Va																288
aac at Asn Il																336
tat at Tyr Il																384
atc cg Ile Ar 13	g His															432
cag ca Gln Gl 145																480
cac ta His Ty																528
cgc ga Arg As																576
ctc gg Leu Gl	_	_		_		_										600

195 200

<210> 43

<211> 200

<212> PRT

<213> Artificial

<220>

<223> modified frag.; YFPF2A with K79R mutation + Met @ posit. 1

<400> 43

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Arg Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190

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<210> 44
<211> 597
<212> DNA
<213>
      Artificial
<220>
<223>
       modified frag.; YFPF2A with Y66F mutation
<220>
<221>
       CDS
<222>
       (1)..(597)
<400> 44
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg
                                                                       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
ccc tgg ccc acc ctc gtg acc acc ttc ggc ttc ggc ctg cag tgc ttc
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Phe Gly Leu Gln Cys Phe
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc
                                                                      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
                            40
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac
                                                                      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50
                        55
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg
                                                                      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac
                                                                      288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat
                                                                      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100
                                105
atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc
                                                                      384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115
                            120
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag
                                                                      432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130
                        135
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac
                                                                      480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145
                    150
                                        155
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc
                                                                      528
```

Leu Gly Met Asp Glu Leu Tyr Lys

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg

165	170	175
100	170	1/3

gat cac Asp His															576
ggc atg Gly Met															597
<211> <212>	45 199 PRT Arti	Eicia	al												
<220> <223>	modi	Eied	frag	g.; 3	/FPF2	2A v	vith	Y66	SF mu	utati	ion				
<400>	45														
Gly Lys 1	Leu	Thr	Leu 5	Lys	Phe	Ile	Cys	Thr 10	Thr	Gly	Lys	Leu	Pro 15	Val	
Pro Trp	Pro	Thr 20	Leu	Val	Thr		Phe 25	Gly	Phe	Gly	Leu	Gln 30	Cys	Phe	
Ala Arg	Tyr 35	Pro	Asp	His	Met	Lys 40	Arg	His	Asp	Phe	Phe 45	Lys	Ser	Ala	
Met Pro 50	Glu	Gly	Tyr	Val	Gln 55	Glu	Arg	Thr	Ile	Phe 60	Phe	Lys	Asp	Asp	
Gly Asn 65	Tyr	Lys	Thr	Arg 70	Ala	Glu	Val	Lys	Phe 75	Glu	Gly	Asp	Thr	Leu 80	
Val Asn	Arg	Ile	Glu 85		Lys	_		_	Phe	_		Asp	Gly 95	Asn	
Ile Leu	Gly	His 100	Lys	Leu	Glu	Tyr	Asn 105	Tyr	Asn	Ser	His	Asn 110	Val	Tyr	
Ile Met	Ala 115	Asp	Lys	Gln	Lys	Asn 120	Gly	Ile	Lys	Val	Asn 125	Phe	Lys	Ile	
Arg His	Asn	Ile	Glu	Asp	Gly 135	Ser	Val	Gln	Leu	Ala 140	Asp	His	Tyr	Gln	
Gln Asn 145	Thr	Pro	Ile	Gly 150	Asp	Gly	Pro	Val	Leu 155	Leu	Pro	Asp	Asn	His 160	

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 46 <211> 600 <212> DNA <213> Artificial <220> <223> modified frag.; YFPF2A with Y66F mutation + Met @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 46 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc ttc ggc ctg cag tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Phe Gly Leu Gln Cys ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly . 85 95 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr

130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 160

cac tac ct His Tyr Le		r Gln Se										528
cgc gat ca Arg Asp Hi												576
ctc ggc atg Leu Gly Me 19	Asp Gl											600
<210> 47 <211> 200 <212> PRT <213> Art	ificial											
<220> <223> mod	ified fr	ag.; YF	F2A 1	with	Y6(6F mi	ıtat:	ion ·	+ Met	t @]	posit. 1	
<400> 47												
Met Gly Lys	Leu Th	r Leu Ly	s Phe	Ile	Cys 10	Thr	Thr	Gly	Lys	Leu 15	Pro	
Val Pro Tr	Pro Th	r Leu Va	l Thr	Thr 25	Phe	Gly	Phe	Gly	Leu 30	Gln	Cys	
Phe Ala Arg	J Tyr Pr	o Asp Hi	s Met 40	Lys	Arg	His	Asp	Phe 45	Phe	Lys	Ser	
Ala Met Pro	Glu Gl	y Tyr Va 55	l Gln	Glu	Arg	Thr	Ile 60	Phe	Phe	Lys	Asp	
Asp Gly Ass 65	ı Tyr Ly	s Thr Ar 70	g Ala	Glu	Val	Lys 75	Phe	Glu	Gly	Asp	Thr 80	
Leu Val Ası	a Arg Il 85	e Glu Le	u Lys	Gly	Ile 90	Asp	Phe	Lys	Glu	Asp 95	Gly	
Asn Ile Leu	Gly Hi 100	s Lys Le	u Glu	Tyr 105	Asn	Tyr	Asn	Ser	His 110	Asn	Val	
Tyr Ile Met		o Lys Gl	n Lys 120	Asn	Gly	Ile	Lys	Val 125	Asn	Phe	Lys	
Ile Arg His	s Asn Il	e Glu As 13		Ser	Val	Gln	Leu 140	Ala	Asp	His	Tyr	

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 170 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 Leu Gly Met Asp Glu Leu Tyr Lys 195 <210> 48 <211> 597 <212> DNA <213> Artificial <220> <223> modified frag.; YFPF2A with Q69K mutation <220> <221> CDS <222> (1)..(597) <400> 48 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg aag tgc ttc 96 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Lys Cys Phe ged ege tad eed gad cad atg aag egg cad gad tto tto aag ted ged 144 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 atg ccc gaa ggc tac gtc caq qaq cqc acc atc ttc ttc aaq qac qac 192 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 90 85 95 atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile

		120	125
		Ser Val Gln Leu	gcc gac cac tac cag 432 Ala Asp His Tyr Gln 140
			ctg ccc gac aac cac 480 Leu Pro Asp Asn His 160
			ccc aac gag aag cgc 528 Pro Asn Glu Lys Arg 175
			gcc ggg atc act ctc 576 Ala Gly Ile Thr Leu 190
ggc atg gac gag Gly Met Asp Glu 195			597
<210> 49 <211> 199 <212> PRT <213> Artificia	ıl		
<220> <223> modified	frag.; YFPF2	A with Q69K mut	tation
<400> 49			
	Leu Lys Phe 5	Ile Cys Thr Thr (Gly Lys Leu Pro Val 15
Gly Lys Leu Thr 1	5	10	
Gly Lys Leu Thr 1 Pro Trp Pro Thr 20	5 Leu Val Thr	Thr Phe Gly Tyr (15 Gly Leu Lys Cys Phe
Gly Lys Leu Thr 1 Pro Trp Pro Thr 20 Ala Arg Tyr Pro 35	5 Leu Val Thr Asp His Met	Thr Phe Gly Tyr (25) Lys Arg His Asp 140 Glu Arg Thr Ile 1	15 Gly Leu Lys Cys Phe 30 Phe Phe Lys Ser Ala
Gly Lys Leu Thr 1 Pro Trp Pro Thr 20 Ala Arg Tyr Pro 35 Met Pro Glu Gly 50	Leu Val Thr Asp His Met Tyr Val Gln 55	Thr Phe Gly Tyr (25) Lys Arg His Asp 140 Glu Arg Thr Ile 1	Gly Leu Lys Cys Phe 30 Phe Phe Lys Ser Ala 45 Phe Phe Lys Asp Asp
Gly Lys Leu Thr 1 Pro Trp Pro Thr 20 Ala Arg Tyr Pro 35 Met Pro Glu Gly 50 Gly Asn Tyr Lys 65	Leu Val Thr Asp His Met Tyr Val Gln 55 Thr Arg Ala 70	Thr Phe Gly Tyr (25) Lys Arg His Asp 140 Glu Arg Thr Ile 16	Gly Leu Lys Cys Phe 30 Phe Phe Lys Ser Ala 45 Phe Phe Lys Asp Asp 60 Glu Gly Asp Thr Leu

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125	
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140	
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160	
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175	
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Gly Met Asp Glu Leu Tyr Lys 195	
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	85	· g	90	95
			aac tac aac agc c Asn Tyr Asn Ser H 1	
	Asp Lys Gln I		ggc atc aag gtg a Gly Ile Lys Val A 125	
			gtg cag ctc gcc g /al Gln Leu Ala A 140	
			ccc gtg ctg ctg c Pro Val Leu Leu E 155	
		Ala Leu S	agc aaa gac ccc a Ser Lys Asp Pro A 170	
			gtg acc gcc gcc g /al Thr Ala Ala G 1	
ctc ggc atg gac Leu Gly Met Asp 195	Glu Leu Tyr I	_		600
210 51				
<210> 51 <211> 200 <212> PRT <213> Artificia	al			
<211> 200 <212> PRT <213> Artificia <220>		A with	O69K mutation +	Met @ posit 1
<211> 200 <212> PRT <213> Artificia <220>		A with	Q69K mutation +	Met @ posit. 1
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Leu	Val	Asn	Arg	Ile 85	Glu	Leu	Lys	Gly	Ile 90	Asp	Phe	Lys	Glu	Asp 95	Gly	
Asn	Ile	Leu	Gly 100	His	Lys	Leu	Glu	Tyr 105	Asn	Tyr	Asn	Ser	His 110	Asn	Val	
Tyr	Ile	Met 115	Ala	Asp	Lys	Gln	Lys 120	Asn	Gly	Ile	Lys	Val 125	Asn	Phe	Lys	
Ile	Arg 130	His	Asn	Ile	Glu	Asp 135	Gly	Ser	Val	Gln	Leu 140	Ala	Asp	His	Tyr	
Gln 145	Gln	Asn	Thr	Pro	Ile 150	Gly	Asp	Gly	Pro	Val 155	Leu	Leu	Pro	Asp	Asn 160	
His	Tyr	Leu	Ser	Tyr 165	Gln	Ser	Ala	Leu	Ser 170	Lys	Asp	Pro	Asn	Glu 175	Lys	•
Arg	Asp	His	Met 180	Val	Leu	Leu		Phe 185	Val	Thr	Ala	Ala	Gly 190	Ile	Thr	
Leu	Gly	Met 195	Asp	Glu	Leu	Tyr	Lys 200									
<210 <211 <212 <213	L> 5 2> I	52 597 ONA Artif	Eicia	al												
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<220 <221 <222	-> (CDS (1)	. (597	7)												
	aag	52 ctg Leu														48
		ccc Pro														96
		tac Tyr 35														144
		gaa Glu														192

	50					55					60					
		tac Tyr														240
		cgc Arg														288
		ggg Gly														336
		gcc Ala 115														384
		aac Asn														432
		acc Thr														480
		agc Ser														528
		atg Met													ctc Leu	576
ggc Gly	atg Met	gac Asp 195	gag Glu	ctg Leu	tac Tyr	aag Lys										597
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<400)> !	53														
Gly 1	Lys	Leu	Thr	Leu 5	Lys	Phe	Ile	Cys	Thr 10	Thr	·Gly	Lys	Leu	Pro 15	Val	
Pro	Trp	Pro	Thr 20	Leu	Val	Thr	Thr	Phe 25	Gly	Tyr	Gly	Leu	Met 30	Cys	Phe	

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 105 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 135 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 54 <211> 600 <212> DNA <213> Artificial <220> <223> modif. frag.; citrine F2A , V68L/ Q69K mutations + Met @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 54 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 10 15

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp

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qtq ccc tqq ccc acc ctc qtg acc acc ttc qqc tac qqc ctq atq tqc
                                                                       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc
                                                                      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac
                                                                      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc
                                                                      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
                                                                      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100
                                105
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag
                                                                      384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac
                                                                      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
                        135
                                                                      480
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                    150
                                        155
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag
                                                                      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165
                                    170
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act
                                                                      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180
                                185
                                                                      600
ctc ggc atg gac gag ctg tac aag
Leu Gly Met Asp Glu Leu Tyr Lys
        195
                            200
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Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys 195 200

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<211> 597

<212> DNA

<213> Artificial

	modif. mutati		_	citi	rine,	/Venu	ısF2 <i>I</i>	4, V6	58L/Ç	Q69K,	/N146	5I/M1	L53T,	/V163A	
	CDS (1)	(597)												
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ccc tgg Pro Trp	Pro 7														96
gcc cgc Ala Arg															144
atg ccc Met Pro 50															192
ggc aac Gly Asn 65															240
gtg aac Val Asn		Ile													288
atc ctg Ile Leu	Gly F														336
atc acc Ile Thr															384
cgc cac Arg His 130															432
cag aac Gln Asn 145															480
tac ctg Tyr Leu		Tyr													528
gat cac Asp His	Met \														576
ggc atg Gly Met															597

<210> 57 <211> 199 <212> PRT <213> Artificial <220> modif. frag.;citrine/VenusF2A, V68L/Q69K/N146I/M153T/V163A <223> mutations <400> 57 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe 25 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 40 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr 100 105 Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 115 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

170

Gly Met Asp Glu Leu Tyr Lys 195 <210> 58 <211> 600 <212> DNA <213> Artificial <220> <223> modif. frag.; citrine/Venus F2A V68L/Q69K/N146I/M153T/V163A mutations + Met @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 58 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 5 gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg atg tgc Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys 25 20 ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 40 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp

55

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc

48

96

144

192

					Thr 70										Thr 80	
					gag Glu											288
		_			aag Lys	_						_				336
					aag Lys											384
					gag Glu											432
					atc Ile 150											480
cac	tac	ctg	agc	tac	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	528
								(66							

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190 600 ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 200 <210> 59 <211> 200 <212> PRT <213> Artificial <220> modif. frag.; citrine/Venus F2A V68L/Q69K/N146I/M153T/V163A <223> mutations + Met @ posit. 1 <400> 59 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 5 10 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys 20 25 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 70 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 95 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 185 Leu Gly Met Asp Glu Leu Tyr Lys 200 <210> 60 <211> 597 <212> DNA <213> Artificial <223> modif. frag.; CFP F2A, F64L mutation <220> <221> CDS <222> (1)..(597) <400> 60 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc ttc 96 Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe 20 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc . 144 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240 Gly Asn Tyr Lys Thr Arq Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn . 85 atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105

384

432

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln

120

130		135	140		
cag aac acc c Gln Asn Thr P 145					
tac ctg agc t Tyr Leu Ser T					
gat cac atg g Asp His Met V 1					
ggc atg gac g Gly Met Asp G 195		_	·		597
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Pro Trp Pro T	Thr Leu Val 1 20	Thr Thr Leu 25	Gly Tyr Gly	Leu Gln Cys 30	Phe
Ala Arg Tyr P	Pro Asp His N	Met Lys Arg 40	His Asp Phe	Phe Lys Ser 45	Ala
Met Pro Glu G 50		Gln Glu Arg 55	Thr Ile Phe 60	Phe Lys Asp	Asp
Gly Asn Tyr L	Lys Thr Arg 1 70	Ala Glu Val	Lys Phe Glu 75	Gly Asp Thr	Leu 80
Val Asn Arg I	Ile Glu Leu I 85	Lys Gly Ile	Asp Phe Lys 90	Glu Asp Gly 95	Asn
Ile Leu Gly H	His Lys Leu (100	Glu Tyr Asn 105	Tyr Asn Ser	His Asn Val	Tyr
Ile Met Ala A 115	Asp Lys Gln 1	Lys Asn Gly 120	Ile Lys Val	Asn Phe Lys 125	Ile

130 135 140	
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160	
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175	
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190	
Gly Met Asp Glu Leu Tyr Lys 195	
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atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1 5 10 15 gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys	
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1 5 10 10 15 gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys 20 25 30 ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser	96
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1 5 10 10 15 gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys 20 25 30 ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp	96 144
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1	96 144 192

100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val As 115 120 125	
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc ga Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala As 130 135 140	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg cc Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pr 145 150 155	
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aa His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro As 165 170	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc gc Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gl 180 185 19	ly Ile Thr
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 195 200	600
<210> 63 <211> 200 <212> PRT	
<213> Artificial	
<213> Artificial <220> <223> modif. frag.; CFP F2A, F64L mutation + Met @ pc <400> 63	osit. 1
<220> <223> modif. frag.; CFP F2A, F64L mutation + Met @ pc	
<220> <223> modif. frag.; CFP F2A, F64L mutation + Met @ pc <400> 63 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Ly	ys Leu Pro 15 eu Gln Cys
<pre><220> <223> modif. frag.; CFP F2A, F64L mutation + Met @ pc <400> 63 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Ly 1</pre>	ys Leu Pro 15 eu Gln Cys
<pre><220> <223> modif. frag.; CFP F2A, F64L mutation + Met @ pc <400> 63 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Ly 1</pre>	vs Leu Pro 15 eu Gln Cys) ne Lys Ser
<pre><220> <223> modif. frag.; CFP F2A, F64L mutation + Met @ pc <400> 63 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Ly 1</pre>	vs Leu Pro 15 eu Gln Cys ne Lys Ser ne Lys Asp

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 120 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 Leu Gly Met Asp Glu Leu Tyr Lys 195 200 <210> 64 <211> 597 <212> DNA <213> Artificial <223> modif. frag.; CFP F2A , Y66W mutation <220> <221> CDS <222> (1)..(597) <400> 64 ggc aag ctg acc ctg aag ttc atc tqc acc acc qqc aaq ctq ccc qtq Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ccc tgg ccc acc ctc gtg acc acc ttc ggc tgg ggc ctg cag tgc ttc 96 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Trp Gly Leu Gln Cys Phe gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu

65	70	75	80
gtg aac cgc atc gag Val Asn Arg Ile Glu 85		p Phe Lys Glu Asp	
atc ctg ggg cac aag Ile Leu Gly His Lys 100			
atc atg gcc gac aag Ile Met Ala Asp Lys 115	cag aag aac ggc at Gln Lys Asn Gly Il 120	c aag gtg aac ttc e Lys Val Asn Phe 125	aag atc 384 Lys Ile
cgc cac aac atc gag Arg His Asn Ile Glu 130			
cag aac acc ccc atc Gln Asn Thr Pro Ile 145			
tac ctg agc tac cag Tyr Leu Ser Tyr Gln 165	tcc gcc ctg agc aa Ser Ala Leu Ser Ly 17	s Asp Pro Asn Glu	aag cgc 528 Lys Arg 175
gat cac atg gtc ctg Asp His Met Val Leu 180			
ggc atg gac gag ctg Gly Met Asp Glu Leu 195	•		597
<210> 65 <211> 199 <212> PRT <213> Artificial			
<220> <223> modif. frag.	; CFP F2A , Y66W m	utation	
<400> 65			
Gly Lys Leu Thr Leu 1 5	Lys Phe Ile Cys Th	r Thr Gly Lys Leu	Pro Val 15
Pro Trp Pro Thr Leu 20	Val Thr Thr Phe Gl 25	y Trp Gly Leu Gln 30	Cys Phe
Ala Arg Tyr Pro Asp 35	His Met Lys Arg Hi 40	s Asp Phe Phe Lys 45	Ser Ala
Met Pro Glu Gly Tyr			

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 90 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 135 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 155 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190 Gly Met Asp Glu Leu Tyr Lys 195 <210> 66 <211> 600 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F2A , Y66W mutation + Met @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 66 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tgg ggc ctg cag tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Trp Gly Leu Gln Cys 20 ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser

35	40	45		
gcc atg ccc gaa ggc t Ala Met Pro Glu Gly T 50				192
gac ggc aac tac aag a Asp Gly Asn Tyr Lys T 65				240
ctg gtg aac cgc atc g Leu Val Asn Arg Ile 6 85				288
aac atc ctg ggg cac a Asn Ile Leu Gly His I 100				336
tat atc atg gcc gac a Tyr Ile Met Ala Asp I 115			l Asn Phe Lys	384
atc cgc cac aac atc g Ile Arg His Asn Ile G 130				432
cag cag aac acc ccc a Gln Gln Asn Thr Pro I 145				480
cac tac ctg agc tac c His Tyr Leu Ser Tyr G 165				528
cgc gat cac atg gtc c Arg Asp His Met Val L 180				576
ctc ggc atg gac gag c Leu Gly Met Asp Glu L 195				600
<210> 67 <211> 200 <212> PRT <213> Artificial				
	CFP F2A , Y66W	mutation + Me	t @ posit. 1	
<400> 67	•			
Met Gly Lys Leu Thr L 1 5	eu Lys Phe Ile	Cys Thr Thr Gly	y Lys Leu Pro 15	

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Trp Gly Leu Gln Cys 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 175 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 Leu Gly Met Asp Glu Leu Tyr Lys

<210> 68
<211> 597
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; CFP F2A , S65A mutation

<220>
<221> CDS
<221> CDS
<222> (1)..(597)
<400> 68

48

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val

1				5					10				15		
											ggc Gly				96
											ttc Phe				144
											ttc Phe 60				192
											gag Glu				240
											aag Lys				288
	_			_	_						agc Ser		_		336
											gtg Val				384
											gcc Ala 140				432
											ctg Leu			cac His 160	480
											ccc Pro				528
											gcc Ala				576
					tac Tyr										597
<210 <211 <212 <213	l> 1 2> E	59 199 PRT Artif	ficia	al											
<220 <223		nodif	f. fr	rag.;	; CFI	P F2#	A , S	565A	mut	atio	on				

<400> 69

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu Gln Cys Phe 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

Gly Met Asp Glu Leu Tyr Lys 195

<210> 70

<211> 600

<212> DNA

<213> Artificial

<22 <22		modi:	f. f	rag.	; CF	P F2	A , A	S65A	mu	tatio	on +	Met	@ pa	osit	1	
<22 <22 <22	1> (CDS	. (60	0)												
	ggc				ctg Leu											48
					ctc Leu											96
					gac Asp											144
					tac Tyr											192
					acc Thr 70											240
					gag Glu											288
					aag Lys											336
					aag Lys											384
					gag Glu											432
					atc Ile 150											480
					cag Gln											528
					ctg Leu											576
					ctg Leu											600

<210> 71

<211> 200

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F2A , S65A mutation + Met @ posit 1

<400> 71

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys

<210 <210 <210 <210	1 > 2 >	72 597 DNA Artii	ficia	al											
<220 <220		modii	f. fi	rag.	; CGI	FP F	2A, S	565A,	/Y66I	N/T2	YEC	muta	ation	ns	
<220 <220 <220	1>	CDS	. (59	7)											
	aag	72 ctg Leu													48
		ccc Pro													· 96
		tac Tyr 35													144
		gaa Glu													192
		tac Tyr													240
		cgc Arg													288
		999 Gly													336
		gcc Ala 115													384
		aac Asn													432
		acc Thr													480
		agc Ser													528

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 597 ggc atg gac gag ctg tac aag Gly Met Asp Glu Leu Tyr Lys 195 <210> 73 <211> 199 <212> PRT <213> Artificial <220> <223> modif. frag.; CGFP F2A, S65A/Y66W/T203Y mutations <400> 73 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Trp Gly Leu Gln Cys Phe 20 25 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 70 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His

155

150

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 74 <211> 600 <212> DNA <213> Artificial <220> <223> modif. frag.; CGFP F2A, S65A/Y66W/T203Y mutations + Met @ pos. 1 <220> <221> CDS <222> (1)..(600) <400> 74 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtg ccc tgg ccc acc ctc gtg acc acc ttc gcc tgg ggc ctg cag tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Trp Gly Leu Gln Cys ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys

432

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr

130	135	140
cag cag aac acc ccc atc Gln Gln Asn Thr Pro Ile 145 150		
cac tac ctg agc tac cag His Tyr Leu Ser Tyr Gln 165		
cgc gat cac atg gtc ctg Arg Asp His Met Val Leu 180		
ctc ggc atg gac gag ctg Leu Gly Met Asp Glu Leu 195		600
<210> 75 <211> 200 <212> PRT <213> Artificial		
<220> <223> modif. frag.; CG	FP F2A, S65A/Y66W/T20	03Y mutations + Met @ pos. 1
<400> 75		
Met Gly Lys Leu Thr Leu 1 5	Lys Phe Ile Cys Thr	Thr Gly Lys Leu Pro 15
Val Pro Trp Pro Thr Leu 20	Val Thr Thr Phe Ala 25	Trp Gly Leu Gln Cys
Phe Ala Arg Tyr Pro Asp 35	His Met Lys Arg His	Asp Phe Phe Lys Ser
Ala Met Pro Glu Gly Tyr 50	Val Gln Glu Arg Thr 55	Ile Phe Phe Lys Asp
Asp Gly Asn Tyr Lys Thr 65 70	Arg Ala Glu Val Lys 75	Phe Glu Gly Asp Thr 80
Leu Val Asn Arg Ile Glu 85	Leu Lys Gly Ile Asp 90	Phe Lys Glu Asp Gly 95
Asn Ile Leu Gly His Lys 100	Leu Glu Tyr Asn Tyr 105	Asn Ser His Asn Val
Tyr Ile Met Ala Asp Lys 115	Gln Lys Asn Gly Ile 120	Lys Val Asn Phe Lys 125

130	e Glu Asp Gly 135	y Ser Val Gln	Leu Ala Asp 140	His Tyr
Gln Gln Asn Thr Pr 145	o Ile Gly As 150	o Gly Pro Val 155	Leu Leu Pro	Asp Asn 160
His Tyr Leu Ser Ty 16		a Leu Ser Lys 170	Asp Pro Asn	Glu Lys 175
Arg Asp His Met Va 180	l Leu Leu Gl	Phe Val Thr	Ala Ala Gly 190	Ile Thr
Leu Gly Met Asp Gl 195	u Leu Tyr Ly: 20			
<210> 76 <211> 597 <212> DNA <213> Artificial	·			
<220> <223> modif. frag mutations	. CGFP F2A ,	F64L/S65T/Y66	5W/M153T/V163	3A/T203Y
<220> <221> CDS <222> (1)(597)				
<221> CDS				
<221> CDS <222> (1)(597) <400> 76 ggc aag ctg acc ct Gly Lys Leu Thr Le	Lys Phe Ile	e Cys Thr Thr 10 c ctg acc tgg	Gly Lys Leu ggc ctg cag	Pro Val 15 tgc ttc 96
<pre><221> CDS <222> (1)(597) <400> 76 ggc aag ctg acc ct Gly Lys Leu Thr Le 1</pre>	c gtg acc acc Val Thr Th	Cys Thr Thr 10 Cctg acc tgg Leu Thr Trp 25 Ccgg cac gac	ggc ctg cag Gly Leu Gln 30 ttc ttc aag	Pro Val 15 tgc ttc 96 Cys Phe tcc gcc 144
<pre><221> CDS <222> (1)(597) <400> 76 ggc aag ctg acc ct Gly Lys Leu Thr Le 1</pre>	c gtg acc acc Val Thr The c cac atg aag His Met Lys 40	Cys Thr Thr 10 C ctg acc tgg Leu Thr Trp 25 C cgg cac gac Arg His Asp	ggc ctg cag Gly Leu Gln 30 ttc ttc aag Phe Phe Lys 45 ttc ttc aag	Pro Val 15 tgc ttc 96 Cys Phe tcc gcc 144 Ser Ala gac gac 192
<pre><221> CDS <222> (1)(597) <400> 76 ggc aag ctg acc ct Gly Lys Leu Thr Le 1</pre>	c gtg acc acc u Val Thr Thi c cac atg aag his Met Lys 40 c gtc cag gag r Val Gln Gln 55	Cys Thr Thr 10 C ctg acc tgg Leu Thr Trp 25 C cgg cac gac Arg His Asp C cgc acc atc Arg Thr Ile	ggc ctg cag Gly Leu Gln 30 ttc ttc aag Phe Phe Lys 45 ttc ttc aag Phe Phe Lys 60 gag ggc gac	Pro Val 15 tgc ttc 96 Cys Phe tcc gcc 144 Ser Ala gac gac 192 Asp Asp acc ctg 240

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 110	336
atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 115 120 125	384
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140	432
cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160	480
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175	528
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190	576
ggc atg gac gag ctg tac aag Gly Met Asp Glu Leu Tyr Lys 195	597
<210> 77 <211> 199 <212> PRT <213> Artificial	
<220> <223> modif. frag. CGFP F2A , F64L/S65T/Y66W/M153T/V163A/T203Y mutations	
<400> 77	
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 1 5 10 15	
Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe 20 25 30	
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45	
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60	

Val	Asn	Arg	Ile	Glu 85	Leu	Lys	Gly	Ile	Asp 90	Phe	Lys	Glu	Asp	Gly 95	Asn	
Ile	Leu	Gly	His 100	Lys	Leu	Glu	Tyr	Asn 105	Tyr	Asn	Ser	His	Asn 110	Val	Tyr	
Ile	Thr	Ala 115	Asp	Lys	Gln	Lys	Asn 120	Gly	Ile	Lys	Ala	Asn 125	Phe	Lys	Ile	
Arg	His 130	Asn	Ile	Glu	Asp	Gly 135	Ser	Val	Gln	Leu	Ala 140	Asp	His	Tyr	Gln	
Gln 145	Asn	Thr	Pro	Ile	Gly 150	Asp	Gly	Pro	Val	Leu 155	Leu	Pro	Asp	Asn	His 160	
Tyr	Leu	Ser	Tyr	Gln 165	Ser	Ala	Leu	Ser	Lys 170	Asp	Pro	Asn	Glu	Lys 175	Arg	
Asp	His	Met	Val 180	Leu	Leu	Glu	Phe	Val 185	Thr	Ala	Ala	Gly	Ile 190	Thr	Leu	
Gly	Met	Asp 195	Glu	Leu	Tyr	Lys										
<210 <211 <212 <213	L> 6 2> I	78 500 ONA Artif	Eicia	al												
<220 <223	3> r	modif mutat							365T/	[/] Y66V	V/M15	53T/\	71,632	A/T20)3Y	
<220 <221 <222	L> (CDS (1)	. (600))												
atg		78 aag Lys														4 8
gtg Val	ccc Pro	tgg Trp	ccc Pro 20	acc Thr	ctc Leu	gtg Val	acc Thr	acc Thr 25	ctg Leu	acc Thr	tgg Trp	ggc Gly	ctg Leu 30	cag Gln	tgc Cys	96
		cgc Arg														144

				atc ttc ttc Ile Phe Phe 60	
				ttc gag ggc Phe Glu Gly	
				ttc aag gag Phe Lys Glu	
		Leu Glu T		aac agc cac Asn Ser His 110	
				aag gcc aac Lys Ala Asn 125	
				ctc gcc gac Leu Ala Asp 140	
		Gly Asp G		ctg ctg ccc Leu Leu Pro	
				gac ccc aac Asp Pro Asn	
		Leu Glu Pl		gcc gcc ggg Ala Ala Gly 190	
	gac gag ctg Asp Glu Leu				600
<210> 79 <211> 200 <212> PRT <213> Artis	ficial				
	f. frag. CGF tions + Met			N/M153T/V163 <i>F</i>	A/T203Y
<400> 79					
Met Gly Lys	Leu Thr Leu 5	Lys Phe I	le Cys Thr 10	Thr Gly Lys	Leu Pro 15
Val Pro Trp	Pro Thr Leu 20	Val Thr Th		Trp Gly Leu 30	Gln Cys

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys 195 200

<210> 80

<211> 597

<212> DNA

<213> Artificial

<220>

<223> modif. frag., CFP F2A, F46L/S65T/Y66W/N146I/M153T/V163A mutations

<220>

<221> CDS

<222> (1)..(597)

<40	30								
			aag Lys						48
			gtg Val						96
			cac His						144
			gtc Val						192
			cgc Arg 70						240
			ctg Leu						288
			ctg Leu						336
			cag Gln						384
			gac Asp						432
			ggc Gly 150						480
			tcc Ser						528
			ctg Leu						576
			tac Tyr						597

<210> 81

<211> 199 <212> PRT <213> Artificial

<220>

<223> modif. frag., CFP F2A, F46L/S65T/Y66W/N146I/M153T/V163A
mutations

<400> 81

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr 100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

Gly Met Asp Glu Leu Tyr Lys 195

<210> 82 <211> 600

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gtg c Val E																96
ttc g Phe A	_	_			_		_	_			_			_		144
gcc a Ala M																192
gac g Asp 6	ggc	aac Asn	tac Tyr	aag Lys	acc Thr 70	cgc Arg	gcc Ala	gag Glu	gtg Val	aag Lys 75	ttc Phe	gag Glu	ggc Gly	gac Asp	acc Thr 80	240
ctg g Leu V																288
aac a Asn I																336
tat a Tyr I																384
atc c Ile A																432
cag c Gln G 145	cag Sln	aac Asn	acc Thr	ccc Pro	atc Ile 150	ggc Gly	gac Asp	ggc Gly	ccc Pro	gtg Val 155	ctg Leu	ctg Leu	ccc Pro	gac Asp	aac Asn 160	480
cac t His T																528
cgc g Arg A																576

ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 195 200

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<211> 200

<212> PRT

<213> Artificial

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 mutations + Met @ posit. 1

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Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

Leu Gly Met Asp Glu Leu Tyr Lys 195 200 <210> 84 <211> 597 <212> DNA <213> Artificial <220> <223> modif. frag. CFP F2A, N146I mutation <220> <221> CDS <222> (1)..(597) <400> 84 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ecc tgg ecc acc etc gtg acc acc tte gge tac gge etg eag tge tte 96 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 95 atc ctg ggg cac aag ctg gag tac aac tac atc aqc cac aac qtc tat 336 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr 100 atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac cac 480 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

185

tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190	576
ggc atg gac gag ctg tac aag Gly Met Asp Glu Leu Tyr Lys 195	597
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Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 30	
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45	
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60	
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80	
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95	
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr 100 105 110	
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125	
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140	
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160	

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 170 165 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 86 <211> 600 <212> DNA <213> Artificial <220> modif. frag. CFP F2A, N146I mutation + Met @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 86 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 10 gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc qac acc 240 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 336 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr

130 135 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac 480 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 150 155 cac tac ctg age ace cag tee gee ctg age aaa gae eee aae gag aag 528 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190 600 ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 195 200 <210> 87 <211> 200 <212> PRT <213> Artificial modif. frag. CFP F2A, N146I mutation + Met @ posit. 1 <223> <400> 87

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Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75. 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 110

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 130 135 140	His Tyr
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 145 150 155	Asp Asn 160
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn o	Glu Lys 175
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 180 185 190	Ile Thr
Leu Gly Met Asp Glu Leu Tyr Lys 195 200	
<210> 88 <211> 597 <212> DNA <213> Artificial	
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gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag all Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys 35 40 45	
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag g Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys 5 50 55 60	
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac a Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 1 65 70 75	acc ctg 240 Thr Leu 80
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac	
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp (95

100 105 110

115	gac aa Asp Ly	g cag s Gln	aag Lys	aac Asn 120	ggc Gly	atc Ile	aag Lys	gtg Val	aac Asn 125	ttc Phe	aag Lys	atc Ile	384
cgc cac aad Arg His Asi 130													432
cag aac acc Gln Asn Thi 145													480
tac ctg ago Tyr Leu Se		n Ser											528
gat cac ato Asp His Met													576
ggc atg gad Gly Met Asp 199	Glu Le												597
<210> 89 <211> 199 <212> PRT <213> Artificial													
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	f. frag	. CFP	F2A,	M15	53T n	nutat	ion						
<223> modi								Gly	Lys	Leu	Pro 15	Val	
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<223> mod: <400> 89 Gly Lys Leu 1	Thr Le 5 Thr Le 20	ı Lys ı Val	Phe Thr	Ile Thr	Cys Phe 25	Thr 10	Thr Tyr	Gly	Leu	Gln 30	15 Cys	Phe	
<223> modified with the second	Thr Le 5 Thr Le 20	ı Lys ı Val	Phe Thr Met	Ile Thr Lys 40	Cys Phe 25 Arg	Thr 10 Gly His	Thr Tyr Asp	Gly	Leu Phe 45	Gln 30 Lys	15 Cys Ser	Phe Ala	
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Ile Leu Gly H	His Lys Leu 100	Glu Tyr As:	-		Asn Val Tyr 110	
Ile Thr Ala A 115	Asp Lys Gln	Lys Asn Gl	y Ile Lys	Val Asn I 125	Phe Lys Ile	
Arg His Asn I	Ile Glu Asp	Gly Ser Va 135	l Gln Leu	Ala Asp H 140	His Tyr Gln	
Gln Asn Thr P	Pro Ile Gly 150	Asp Gly Pro	o Val Leu 155	Leu Pro A	Asp Asn His 160	
Tyr Leu Ser T	Thr Gln Ser 165	Ala Leu Se	r Lys Asp 170	Pro Asn G	Glu Lys Arg 175	
Asp His Met V	Val Leu Leu .80	Glu Phe Va		_	lle Thr Leu 190	
Gly Met Asp G 195	Glu Leu Tyr	Lys				
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<220> <223> modif.	frag. CFP	F2A, M153T	mutation	+ Met @ p	posit. 1	
<220> <221> CDS <222> (1)((600)					
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gtg ccc tgg c Val Pro Trp P 2				Tyr Gly I		
ttc gcc cgc t Phe Ala Arg T 35						144
gcc atg ccc g Ala Met Pro G 50						192

gac ggc aac Asp Gly Asn 65							
ctg gtg aac Leu Val Asn				_			
aac atc ctg Asn Ile Leu							
tat atc acc Tyr Ile Thr 115							
atc cgc cac Ile Arg His 130					Ala Asp		
cag cag aac Gln Gln Asn 145		e Gly Asp					ı
cac tac ctg His Tyr Leu				_			•
cgc gat cac Arg Asp His							
ctc ggc atg Leu Gly Met 195		_					600
<210> 91 <211> 200 <212> PRT <213> Artif	icial						·
<220> <223> modif	. frag. CF	P F2A, M1	53T muta	tion + M	et @ pos	it. 1	
<400> 91			•				
Met Gly Lys 1	Leu Thr Le	Lys Phe	Ile Cys	Thr Thr	Gly Lys	Leu Pro	
Val Pro Trp	Pro Thr Le	ı Val Thr	Thr Phe 25	Gly Tyr	Gly Leu 30	Gln Cys	3
Phe Ala Arg	Tyr Pro As	His Met	Lys Arg	His Asp	Phe Phe	Lys Ser	•

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 55 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 70 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 120 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 Leu Gly Met Asp Glu Leu Tyr Lys 200 <210> 92 <211> 597 <212> DNA <213> Artificial <223> modif. frag. CFP F2A, N146I/ M153T mutations <220> <221> CDS <222> (1)..(597) ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe

				20					25					30			
												ttc Phe					144
												ttc Phe 60					192
												gag Glu					240
												aag Lys					288
												agc Ser					336
												gtg Val					384
*												gcc Ala 140					432
												ctg Leu					480
												ccc Pro					528
			Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Āla	gcc Ala	Gly	Ile	Thr		576
			gac Asp 195														597
	<210 <211 <212 <213	L> 1 2> I	93 199 PRT Artif	ficia	al												

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 1 5 10 15

<223> modif. frag. CFP F2A, N146I/ M153T mutations

<220>

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 40 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 70 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr 100 105 Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 150 Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 94 <211> 600 <212> DNA <213> Artificial <220> <223> modif. frag. CFP F2A, N146I/ M153T mutations + Met @ posit. 1 <220> <221> CDS

<222> (1)..(600)

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gt Va	g ccc l Pro	tgg Trp	ccc Pro 20	acc Thr	ctc Leu	gtg Val	acc Thr	acc Thr 25	ttc Phe	ggc Gly	tac Tyr	ggc Gly	ctg Leu 30	cag Gln	tgc Cys	9	6
tt Ph	c gcc e Ala	cgc Arg 35	tac Tyr	ccc Pro	gac Asp	cac His	atg Met 40	aag Lys	cgg Arg	cac His	gac Asp	ttc Phe 45	ttc Phe	aag Lys	tcc Ser	14	4
gc Al	c atg a Met 50	ccc Pro	gaa Glu	ggc Gly	tac Tyr	gtc Val 55	cag Gln	gag Glu	cgc Arg	acc Thr	atc Ile 60	ttc Phe	ttc Phe	aag Lys	gac Asp	19	2
ga As 65	c ggc p Gly	aac Asn	tac Tyr	aag Lys	acc Thr 70	cgc Arg	gcc Ala	gag Glu	gtg Val	aag Lys 75	ttc Phe	gag Glu	ggc Gly	gac Asp	acc Thr 80	24	0
ct Le	g gtg u Val	aac Asn	cgc Arg	atc Ile 85	gag Glu	ctg Leu	aag Lys	ggc Gly	atc Ile 90	gac Asp	ttc Phe	aag Lys	gag Glu	gac Asp 95	ggc Gly	28	8
aa As	c atc n Ile	ctg Leu	999 Gly 100	cac His	aag Lys	ctg Leu	gag Glu	tac Tyr 105	aac Asn	tac Tyr	atc Ile	agc Ser	cac His 110	aac Asn	gtc Val	33	6
ta Ty	t atc r Ile	acc Thr 115	gcc Ala	gac Asp	aag Lys	cag Gln	aag Lys 120	aac Asn	ggc Gly	atc Ile	aag Lys	gtg Val 125	aac Asn	ttc Phe	aag Lys	384	4
	c cgc e Arg 130															43	2
ca Gl: 14	g cag n Gln	aac Asn	acc Thr	ccc Pro	atc Ile 150	ggc Gly	gac Asp	ggc Gly	ccc Pro	gtg Val 155	ctg Leu	ctg Leu	ccc Pro	gac Asp	aac Asn 160	480	0
ca:	c tac s Tyr	ctg Leu	agc Ser	acc Thr 165	cag Gln	tcc Ser	gcc Ala	ctg Leu	agc Ser 170	aaa Lys	gac Asp	ccc Pro	aac Asn	gag Glu 175	aag Lys	528	3
cg Ar	c gat g Asp	cac His	atg Met 180	gtc Val	ctg Leu	ctg Leu	gag Glu	ttc Phe 185	gtg Val	acc Thr	gcc Ala	gcc Ala	999 Gly 190	atc Ile	act Thr	576	5
	ggc Gly															600)

<210> 95

<211> 200

<212> PRT

<213> Artificial

<220>

<223> modif. frag. CFP F2A, N146I/ M153T mutations + Met @ posit. 1 $\,$

<400> 95

Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 1 5 10 15

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys

195 200

<21: <21: <21: <21:	1> 2>	96 597 DNA Arti:	ficia	al												
<22 <22	3 >	modi: muta			; CF	P F2	A, F	64L/8	S65T,	/Y66I	W/N1	461/1	M153'	r		
<22) <22) <22)	1>	CDS (1).	. (59°	7)												
	aag	96 ctg Leu														48
		ccc Pro														96
		tac Tyr 35														144
		gaa Glu														192
		tac Tyr														240
gtg Val	aac Asn	cgc Arg	atc Ile	gag Glu 85	ctg Leu	aag Lys	ggc Gly	atc Ile	gac Asp 90	ttc Phe	aag Lys	gag Glu	gac Asp	ggc Gly 95	aac Asn	288
atc Ile	Leu	ggg Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Ile	Ser	His	Asn	Val	tat Tyr	336
		gcc Ala 115														384
		aac Asn														432
		acc Thr														480
		agc Ser														528

165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

576

ggc atg gac gag ctg tac aag Gly Met Asp Glu Leu Tyr Lys 195 597

<210> 97 <211> 199

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<220>

<223> modif. frag.; CFP F2A, F64L/S65T/Y66W/N146I/M153T mutations

<400> 97

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val 1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe 20 25 30 ·

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35° 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

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Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg

atc cgc cac aa Ile Arg His As 130								432
cag cag aac ac Gln Gln Asn Th 145								480
cac tac ctg ag His Tyr Leu Se								528
cgc gat cac at Arg Asp His Me 18	et Val Leu					Ile		576
ctc ggc atg ga Leu Gly Met As 195								600
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Met Gly Lys Le	5 Thr Leu		Ile Cys 10			15		
Met Gly Lys Le	5 	Val Thr	Ile Cys 10 Thr Leu 25	Thr Trp	Gly Leu 30	15 Gln	Cys	
Met Gly Lys Le	5 TO Thr Leu or Pro Asp	Val Thr His Met	Ile Cys 10 Thr Leu 25	Thr Trp	Gly Leu 30 Phe Phe 45	15 Gln Lys	Cys Ser	
Met Gly Lys Legal 1 Val Pro Trp Pro 20 Phe Ala Arg Ty 35 Ala Met Pro Gl	o Thr Leu r Pro Asp	Val Thr His Met 40 Val Gln 55	Ile Cys 10 Thr Leu 25 Lys Arg	Thr Trp His Asp Thr Ile 60	Gly Leu 30 Phe Phe 45 Phe Phe	Gln Lys Lys	Cys Ser Asp	
Met Gly Lys Legal 1 Val Pro Trp Pro 20 Phe Ala Arg Ty 35 Ala Met Pro Gl So Asp Gly Asn Ty	o Thr Leu r Pro Asp u Gly Tyr r Lys Thr 70	Val Thr His Met 40 Val Gln 55 Arg Ala	Ile Cys 10 Thr Leu 25 Lys Arg Glu Arg	Thr Trp His Asp Thr Ile 60 Lys Phe 75	Gly Leu 30 Phe Phe 45 Phe Phe Glu Gly	Gln Lys Lys	Cys Ser Asp Thr	

Tyr Ile Thr 115	Ala Asp I	Lys Gln Ly: 12	_	Ile Lys	Val Asn 125	Phe Lys	
Ile Arg His 130	Asn Ile (Glu Asp Gly 135	y Ser Val	Gln Leu 140	Ala Asp	His Tyr	
Gln Gln Asn 145		Ile Gly As _l 150	Gly Pro	Val Leu 155	Leu Pro	Asp Asn 160	
His Tyr Leu	Ser Thr (Gln Ser Ala	a Leu Ser 170	_	Pro Asn	Glu Lys 175	
Arg Asp His	Met Val I 180	Leu Leu Glı	ı Phe Val 185	Thr Ala	Ala Gly 190	Ile Thr	
Leu Gly Met 195	Asp Glu I	Leu Tyr Ly: 20					
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Met Pro Giu 50	Gly Tyr V	55	9	60	1110 1170		

gtg aac cgc Val Asn Arg							y Asn	288
atc ctg ggg Ile Leu Gly								336
atc atg gcc Ile Met Ala 115								384
cgc cac aac Arg His Asn 130								432
cag aac acc Gln Asn Thr 145	Pro Ile				Leu Pro			480
tac ctg agc Tyr Leu Ser	acc cag Thr Gln 165	tcc gcc Ser Ala	ctg agc Leu Ser	aaa gac Lys Asp 170	ccc aac Pro Asn	gag aa Glu Ly 17	s Arg	528
gat cac atg Asp His Met								576
ggc atg gac Gly Met Asp 195								597
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Pro Trp Pro	Thr Leu 20	Val Thr	Thr Phe 25	Gly Tyr	Gly Leu	Gln Cy 30	s Phe	
Ala Arg Tyr 35	Pro Asp	His Met	Lys Arg 40	His Asp	Phe Phe 45	Lys Se	r Ala	
Met Pro Glu 50	Gly Tyr	Val Gln 55	Glu Arg	Thr Ile	Phe Phe	Lys As	p Asp	

Gly 65	Asn	Tyr :	Lys	Thr	Arg 70	Ala	Glu	Val	Lys	Phe 75	Glu	Gly	Asp	Thr	Leu 80	
Val	Asn	Arg	Ile	Glu 85	Leu	Lys	Gly	Ile	Asp 90	Phe	Lys	Glu	Asp	Gly 95	Asn	
Ile	Leu	Gly	His 100	Lys	Leu	Glu	Tyr	Asn 105	Tyr	Asn	Ser	His	Asn 110	Val	Tyr	
Ile	Met	Ala 115	Asp	Lys	Gln	Lys	Asn 120	Gly	Ile	Lys	Ala	Asn 125	Phe	Lys	Ile	
Arg	His 130	Asn	Ile	Glu	Asp	Gly 135	Ser	Val	Gln	Leu	Ala 140	Asp	His	Tyr	Gln	
Gln 145	Asn	Thr	Pro	Ile	Gly 150	Asp	Gly	Pro	Val	Leu 155	Leu	Pro	Asp	Asn	His 160	
Tyr	Leu	Ser	Thr	Gln 165	Ser	Ala	Leu	Ser	Lys 170	Asp	Pro	Asn	Glu	Lys 175	Arg	
Asp	His	Met	Val 180	Leu	Leu	Glu	Phe	Val 185	Thr	Ala	Ala	Gly	Ile 190	Thr	Leu	
Gly	Met	Asp 195	Glu	Leu	Tyr	Lys										
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				acc Thr												96
				ccc Pro												144

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					tac Tyr								192
					acc Thr 70								240
					gag Glu								288
		-	_		aag Lys	_				_		_	336
					aag Lys								384
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					atc Ile 150								480
					cag Gln								528
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Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 55 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 150 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 190 Leu Gly Met Asp Glu Leu Tyr Lys <210> 104 <211> 597 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F2A, N146I/ V163A mutations <220> <221> CDS <222> (1)..(597)

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			atc ttc ttc aa Ile Phe Phe Ly 60	
			ttc gag ggc ga Phe Glu Gly As 75	
			ttc aag gag ga Phe Lys Glu As	
	s Lys Leu Glu		atc agc cac aa Ile Ser His As 11	n Val Tyr
			aag gcc aac tt Lys Ala Asn Ph 125	
			ctc gcc gac ca Leu Ala Asp Hi 140	
			ctg ctg ccc ga Leu Leu Pro As 155	
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Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr 100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

Gly Met Asp Glu Leu Tyr Lys

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gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc
                                                                       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20
                                25
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc
                                                                      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac
                                                                      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
                        55
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc
                                                                      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85
aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc
                                                                      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag
                                                                      384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
        115
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac
                                                                      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130
                        135
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac
                                                                      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145
cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag
                                                                      528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165
                                    170
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155

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 185 Leu Gly Met Asp Glu Leu Tyr Lys 195 <210> 108 <211> 597 <212> DNA <213> Artificial <220> <223> modif. fraq.; CFP F2A, M153T/V163A mutations <220> <221> CDS <222> (1)..(597) <400> 108 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ecc tgg ecc acc etc gtg acc acc tte gge tac gge etg eag tge tte Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe ged ege tad eec gad eac atg aag egg dad gad tid tid aag ted ged 144 Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc 384 Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 115 120

432

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln

130	135	140
cag aac acc ccc atc ggc Gln Asn Thr Pro Ile Gly 145	Asp Gly Pro Val Leu	
tac ctg agc acc cag tcc Tyr Leu Ser Thr Gln Ser 165		
gat cac atg gtc ctg ctg Asp His Met Val Leu Leu 180		
ggc atg gac gag ctg tac Gly Met Asp Glu Leu Tyr 195		
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Ala Arg Tyr Pro Asp His	Met Lys Arg His Asp 40	Phe Phe Lys Ser Ala 45
Met Pro Glu Gly Tyr Val 50	Gln Glu Arg Thr Ile 55	Phe Phe Lys Asp Asp 60
Gly Asn Tyr Lys Thr Arg	Ala Glu Val Lys Phe 75.	Glu Gly Asp Thr Leu 80
Val Asn Arg Ile Glu Leu 85	Lys Gly Ile Asp Phe 90	Lys Glu Asp Gly Asn 95
Ile Leu Gly His Lys Leu 100	Glu Tyr Asn Tyr Asn 105	Ser His Asn Val Tyr
Ile Thr Ala Asp Lys Gln 115	Lys Asn Gly Ile Lys 120	Ala Asn Phe Lys Ile

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140	
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160	
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175	
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190	
Gly Met Asp Glu Leu Tyr Lys 195	
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		age gtg cag ctc go Ser Val Gln Leu Al 140	
		ggc ccc gtg ctg ct Gly Pro Val Leu Le 155	
	nr Gln Ser Ala	ctg agc aaa gac co Leu Ser Lys Asp Pr 170	
		ttc gtg acc gcc gc Phe Val Thr Ala Al 185	
ctc ggc atg gac ga Leu Gly Met Asp Gl 195			600
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Val Pro Trp Pro Tr 20	nr Leu Val Thr	Thr Phe Gly Tyr Gl 25	y Leu Gln Cys 30
Phe Ala Arg Tyr Pr 35	o Asp His Met	Lys Arg His Asp Ph 45	
Ala Met Pro Glu Gl 50	y Tyr Val Gln 55	Glu Arg Thr Ile Ph 60	ne Phe Lys Asp
Asp Gly Asn Tyr Ly 65	s Thr Arg Ala 70	Glu Val Lys Phe Gl 75	u Gly Asp Thr 80
Leu Val Asn Arg Il			

Asn Ile Leu	Gly His	Lys Leu	Glu Tyr 105		Asn Se	r His 110	Asn	Val	
Tyr Ile Thr		Lys Gln	Lys Asn 120	Gly Ile	Lys Al 12		Phe	Lys	
Ile Arg His	Asn Ile	Glu Asp 135	Gly Ser	Val Gln	Leu Al 140	a Asp	His	Tyr	
Gln Gln Asn 145	Thr Pro	Ile Gly 150	Asp Gly	Pro Val 155		u Pro	Asp	Asn 160	
His Tyr Leu	Ser Thr 165	Gln Ser	Ala Leu	Ser Lys 170	Asp Pr	o Asn	Glu 175	Lys	
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Leu Gly Met 195		Leu Tyr	Lys 200						
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gcc cgc tac Ala Arg Tyr 35									144
33									
atg ccc gaa Met Pro Glu 50									192

65	70	75		80
gtg aac cgc atc gag Val Asn Arg Ile Glu 85				
atc ctg ggg cac aag Ile Leu Gly His Lys 100				
atc acc gcc gac aag Ile Thr Ala Asp Lys 115				
cgc cac aac atc gag Arg His Asn Ile Glu 130				
cag aac acc ccc atc Gln Asn Thr Pro Ile 145				
tac ctg agc acc cag Tyr Leu Ser Thr Gln 165			-	_
gat cac atg gtc ctg Asp His Met Val Leu 180				
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Ala Arg Tyr Pro Asp 35	His Met Lys 40	Arg His Asp	Phe Phe Lys Ser	Ala
Met Pro Glu Gly Tyr	Val Gln Glu 55	Arg Thr Ile	Phe Phe Lys Asp	Asp

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 70 65 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 90 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr 105 Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 120 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 135 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 150 155 Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 170 165 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190 Gly Met Asp Glu Leu Tyr Lys 195 <210> 114 <211> 600 <212> DNA <213> Artificial <220> modif. frag.; CFP F2A, N146I/M153T/V163A mutations <223> and Met added @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 114 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro 10 gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45	144
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60	192
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80	240
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95	288
aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 110	336
tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 125	384
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cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	480
cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	528
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Leu Gly Met Asp Glu Leu Tyr Lys 195 200

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		tac Tyr 35															144
		gaa Glu															192
ggc Gly 65	aac Asn	tac Tyr	aag Lys	acc Thr	cgc Arg 70	gcc Ala	gag Glu	gtg Val	aag Lys	ttc Phe 75	gag Glu	ggc Gly	gac Asp	acc Thr	ctg Leu 80		240
		cgc Arg															288
		Gly 999															336
		gcc Ala 115															3'84
		aac Asn															432
		acc Thr															480
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gat Asp	cac His	atg Met	gtc Val 180	ctg Leu	ctg Leu	gag Glu	ttc Phe	gtg Val 185	acc Thr	gcc Ala	gcc Ala	ggg Gly	atc Ile 190	act Thr	ctc Leu	576
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Ala	Arg	Tyr 35	Pro	Asp	His	Met	Lys 40	Arg	His	Asp	Phe	Phe 45	Lys	Ser	Ala	
Met	Pro 50	Glu	Gly	Tyr	Val	Gln 55	Glu	Arg	Thr	Ile	Phe 60	Phe	Lys	Asp	Asp	
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Val	Asn	Arg	Ile	Glu 85	Leu	_	_	Ile	_		Lys	Glu	Asp	Gly 95	Asn	
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Ile	Thr	Ala 115	Asp	Lys	Gln	Lys	Asn 120	Gly	Ile	Lys	Ala	Asn 125	Phe	Lys	Ile	
Arg	His 130	Asn	Ile	Glu	Asp	Gly 135	Ser	Val	Gln	Leu	Ala 140	Asp	His	Tyr	Gln	
Gln 145	Asn	Thr	Pro	Ile	Gly 150	Asp	Gly	Pro	Val	Leu 155	Leu	Pro	Asp	Asn	His 160	

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Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arq

Ile Arg His			Gly Se	gtg cag Val Gln				32
cag cag aac Gln Gln Asn 145								80
cac tac ctg His Tyr Leu							u Lys	28
cgc gat cac Arg Asp His				Val Thr				76
ctc ggc atg Leu Gly Met 195	Asp Glu						6	00
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Met Gly Lys 1 Val Pro Trp Phe Ala Arg	Pro Thr 20 Tyr Pro	Leu Val	Thr Thr 25 Met Lys 40	10 Leu Thr	Trp Gly Asp Phe	Leu Gl 30	n Cys s Ser	
Met Gly Lys 1 Val Pro Trp Phe Ala Arg 35 Ala Met Pro	Pro Thr 20 Tyr Pro Glu Gly	Leu Val Asp His Tyr Val	Thr Thr 25 Met Lys 40 Gln Glu	Leu Thr Arg His	Trp Gly Asp Phe 45 Ile Phe 60	Leu Gl 30 Phe Ly	n Cys s Ser s Asp	
Met Gly Lys Val Pro Trp Phe Ala Arg 35 Ala Met Pro 50 Asp Gly Asn	Pro Thr 20 Tyr Pro Glu Gly Tyr Lys	Leu Val Asp His Tyr Val 55 Thr Arg 70	Thr Thr 25 Met Lys 40 Gln Glu Ala Glu	Leu Thr Arg His Arg Thr Val Lys	Trp Gly Asp Phe 45 Ile Phe 60 Phe Glu	Leu Gl 30 Phe Ly Phe Ly	n Cys s Ser s Asp p Thr 80	

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 125
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190
Leu Gly Met Asp Glu Leu Tyr Lys 195 200
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atc atg gcc gac Ile Met Ala Asp 115	Lys Gln Lys			
cgc cac aac atc Arg His Asn Ile 130				
cag aac acc ccc Gln Asn Thr Pro 145				
tac ctg agc tac Tyr Leu Ser Tyr			Pro Asn Glu L	
gat cac atg gtc Asp His Met Val 180				
ggc atg gac gag Gly Met Asp Glu 195				597
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Pro Trp Pro Thr 20 Ala Arg Tyr Pro	Leu Val Thr	Thr Phe Gly Tyr 25 Lys Arg His Asp	Gly Lys Leu P 1 Gly Leu Gln C 30 Phe Phe Lys S 45	5 ys Phe er Ala

Val	Asn	Arg	Ile	Glu 85	Leu	Lys	Gly	Ile	Asp 90	Phe	Lys	Glu	Asp	Gly 95	Asn	
Ile	Leu	Gly	His 100	Lys	Leu	Glu	Tyr	Asn 105	Tyr	Ile	Ser	His	Asn 110	Val	Tyr	
Ile	Met	Ala 115	Asp	Lys	Gln	Lys	Asn 120	Gly	Ile	Lys	Val	Asn 125	Phe	Lys	Ile	
Arg	His 130	Asn	Ile	Glu	Asp	Gly 135	Ser	Val	Gln	Leu	Ala 140	Asp	His	Tyr	Gln	
Gln 145	Asn	Thr	Pro	Ile	Gly 150	Asp	Gly	Pro	Val	Leu 155	Leu	Pro	Asp	Asn	His 160	
Tyr	Leu	Ser	Tyr	Gln 165	Ser	Ala	Leu	Ser	Lys 170	Asp	Pro	Asn	Glu	Lys 175	Arg	
Asp	His	Met	Val 180	Ľeu	Leu	Glu	Phe	Val 185	Thr	Ala	Ala	Gly	Ile 190	Thr	Leu	
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		tgg Trp														96
		cgc Arg 35														144
		ccc Pro														192

50 55 60

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			gac ttc aag gag Asp Phe Lys Glu	
	y His Lys Lev		tac atc agc cac Tyr Ile Ser His 110	
			atc aag gtg aac Ile Lys Val Asn 125	
		Gly Ser Val	cag ctc gcc gac Gln Leu Ala Asp 140	
			gtg ctg ctg ccc Val Leu Leu Pro 155	
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	t Val Leu Leu		acc gcc gcc ggg Thr Ala Ala Gly 190	
ctc ggc atg ga Leu Gly Met As 195		_		
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Phe Ala Arg Ty	r Pro Asp His	Met Lys Arg	His Asp Phe Phe	Lys Ser

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 55 60 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 75 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 150 155 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 Leu Gly Met Asp Glu Leu Tyr Lys <210> 124 <211> 597 <212> DNA <213> Artificial <220> <223> modif. frag.; CGFP F2A, M153T/T203Y mutations <220> <221> CDS <222> (1)..(597) ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe

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atg ccc gaa Met Pro Glu 50												192
ggc aac tad Gly Asn Tyn 65												240
gtg aac cgo Val Asn Aro												288
atc ctg ggg												336
atc acc gcc Ile Thr Ala 115	a Asp Lys											384
cgc cac aad Arg His Asi 130												432
cag aac acc Gln Asn Thi 145												480
tac ctg ago Tyr Leu Sei		Ser Ala										528
gat cac ato Asp His Met		Leu Glu		Val	Thr	Ăla				Thr		576
ggc atg gad Gly Met Asp 199	Glu Leu											597
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Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

Gly Met Asp Glu Leu Tyr Lys 195

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gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc
                                                                       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20
                                25
tto goo ogo tao ooo gao oac atg aag ogg cao gao tto tto aag too
                                                                      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac
                                                                      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
                                                                      240
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
                                                                      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100
tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag
                                                                      384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115
                            120
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac
                                                                      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130
                        135
caq caq aac acc ccc atc qqc qac qqc ccc qtq ctq ctq ccc qac aac
                                                                      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145
cac tac ctg age tac cag tee gee ctg age aaa gae eee aac gag aag
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His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165
                                     170
                                                                      576
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Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190

Leu Gly Met Asp Glu Leu Tyr Lys 195 200

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		ccc Pro														96
		tac Tyr 35														144
		gaa Glu														192
		tac Tyr														240
		cgc Arg														288
		ggg Gly														336
atc Ile	acc Thr	gcc Ala 115	gac Asp	aag Lys	cag Gln	aag Lys	aac Asn 120	ggc Gly	atc Ile	aag Lys	gtg Val	aac Asn 125	ttc Phe	aag Lys	atc Ile	384
		aac Asn														432

cag aac ac Gln Asn Th 145					Leu Pro		
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gat cac at Asp His Me				Thr Ala			
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Pro Trp Pr	o Thr Leu 20	Val Thr	Thr Phe 25	Gly Tyr	Gly Leu	Gln Cys 30	Phe
Ala Arg Ty	r Pro Asp	His Met	Lys Arg 40	His Asp	Phe Phe 45	Lys Ser	Ala
Met Pro Gl 50	ı Gly Tyr	Val Gln 55	Glu Arg	Thr Ile	Phe Phe	Lys Asp	Asp
Gly Asn Ty 65	r Lys Thr	Arg Ala 70	Glu Val	Lys Phe	Glu Gly	Asp Thr	Leu 80
Val Asn Ar	g Ile Glu 85	Leu Lys	Gly Ile	Asp Phe	Lys Glu	Asp Gly 95	Asn
Ile Leu Gl	y His Lys 100	Leu Glu	Tyr Asn 105	-	Ser His	Asn Val	Tyr
Ile Thr Al		Gln Lys	Asn Gly	Ile Lys	Val Asn 125	Phe Lys	Ile

130	Glu Asp	Gly Ser 135	Val Gln	Leu Ala 140	Asp His	Tyr (31n
Gln Asn Thr Pro	Ile Gly 150	Asp Gly	Pro Val	Leu Leu 155	Pro Asp		His 160
Tyr Leu Ser Tyr	Gln Ser 165	Ala Leu	Ser Lys 170	_	Asn Glu	Lys 1	Arg
Asp His Met Val		Glu Phe	Val Thr 185	Ala Ala	Gly Ile 190	Thr 1	Leu
Gly Met Asp Glu 195	Leu Tyr	Lys					
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	rag.; CG added @ p		146I/ M1	53T/T203	Y mutatio	ons	
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aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 110	336
tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125	384
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140	432
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	480
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	528
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190	576
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 195 200	600
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Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 20 25 30	
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45	
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60	

Leu	Val	Asn	Arg	Ile 85	Glu	Leu	Lys	Gly	Ile 90	Asp	Phe	Lys	Glu	Asp 95	Gly		
Asn	Ile	Leu	Gly 100	His	Lys	Leu	Glu	Tyr 105	Asn	Tyr	Ile	Ser	His 110	Asn	Val		
Tyr	Ile	Thr 115	Ala	Asp	Lys	Gln	Lys 120	Asn	Gly	Ile	Lys	Val 125	Asn	Phe	Lys		
Ile	Arg 130	His	Asn	Ile	Glu	Asp 135	Gly	Ser	Val	Gln	Leu 140	Ala	Asp	His	Tyr		
Gln 145	Gln	Asn	Thr	Pro	Ile 150	Gly	Asp	Gly	Pro	Val 155	Leu	Leu	Pro	Asp	Asn 160	*	
His	Tyr	Leu	Ser	Tyr 165	Gln	Ser	Ala	Leu	Ser 170	Lys	Asp	Pro	Asn	Glu 175	Lys		
Arg	Asp	His	Met 180	Val	Leu	Leu	Glu	Phe 185	Val	Thr	Ala	Ala	Gly 190	Ile	Thr		
Leu	Gly	Met 195	Asp	Glu	Leu	Tyr	Lys 200										
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					gtg Val											S	96
					cac His											14	. 4

			ggc Gly													192
			aag Lys													240
			atc Ile													288
			cac His 100													336
			gac Asp													384
_			atc Ile		_		_		_		_	_			_	432
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			gtc Val 180													576
	_	_	gag Glu	_		_										597
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Gly 1	Lys	Leu	Thr	Leu 5	Lys	Phe	Ile	Cys	Thr 10	Thr	Gly	Lys	Leu	Pro 15	Val	
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Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

55

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr 100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

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Gly Met Asp Glu Leu Tyr Lys 195

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						gtg Val										96
						cac His										144
gcc Ala	atg Met 50	ccc Pro	gaa Glu	ggc Gly	tac Tyr	gtc Val 55	cag Gln	gag Glu	cgc Arg	acc Thr	atc Ile 60	ttc Phe	ttc Phe	aag Lys	gac Asp	192
						cgc Arg										240
						ctg Leu										288
						ctg Leu										336
						cag Gln										384
						gac Asp 135									tac Tyr	432
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						tcc Ser										528
						ctg Leu										576
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Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys
20 25 30

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 . 55 60

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 110

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
115 120 125

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190

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Leu Gly Met Asp Glu Leu Tyr Lys

165	170	175
100	1,0	1/3

			102					1/0					1/5		
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ggc atg Gly Met															597
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Gly Lys 1	Leu :	Thr	Leu 5	Lys	Phe	Ile	Cys	Thr 10	Thr	Gly	Lys	Leu	Pro 15	Val	
Pro Trp		Thr 20	Leu	Val	Thr	Thr	Phe 25	Gly	Tyr	Gly	Leu	Gln 30	Cys	Phe	
Ala Arg	Tyr 1	Pro	Asp	His	Met	Lys 40	Arg	His	Asp	Phe	Phe 45	Lys	Ser	Ala	
Met Pro 50	Glu (Gly	Tyr	Val	Gln 55	Glu	Arg	Thr	Ile	Phe 60	Phe	Lys	Asp	Asp	
Gly Asn 65	Tyr 1	Lys	Thr	Arg 70	Ala	Glu	Val	Lys	Phe 75	Glu	Gly	Asp	Thr	Leu 80	
Val Asn	Arg :	Ile	Glu 85	Leu	Lys	Gly	Ile	Asp 90	Phe	Lys	Glu	Asp	Gly 95	Asn	
Ile Leu		His 100	Lys	Leu	Glu	Tyr	Asn 105	Tyr	Asn	Ser	His	Asn 110	Val	Tyr	
Ile Met	Ala <i>i</i> 115	Asp	Lys	Gln	Lys	Asn 120	Gly	Ile	Lys	Ala	Asn 125	Phe	Lys	Ile	

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

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432

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr

130	135	14	40	
cag cag aac acc ccc Gln Gln Asn Thr Pro 145				
cac tac ctg agc tac His Tyr Leu Ser Tyr 165				
cgc gat cac atg gtc Arg Asp His Met Val 180	Leu Leu Glu Pl			
ctc ggc atg gac gag Leu Gly Met Asp Glu 195				600
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Val Pro Trp Pro Thr 20	Leu Val Thr Ti 2!		yr Gly Leu Gln 30	Cys
Phe Ala Arg Tyr Pro 35	Asp His Met Ly	ys Arg His As	sp Phe Phe Lys 45	Ser
Ala Met Pro Glu Gly 50	Tyr Val Gln G	lu Arg Thr II		Asp
Asp Gly Asn Tyr Lys 65	Thr Arg Ala G	lu Val Lys Pl 75	he Glu Gly Asp	Thr 80
Leu Val Asn Arg Ile 85	Glu Leu Lys G	ly Ile Asp Ph 90	he Lys Glu Asp 95	Gly
Asn Ile Leu Gly His 100		yr Asn Tyr As D5	sn Ser His Asn 110	Val
Tyr Ile Met Ala Asp 115	Lys Gln Lys As	sn Gly Ile Ly	ys Ala Asn Phe 125	Lys

Ile	Arg 130	His	Asn	Ile	Glu	Asp 135	Gly	Ser	Val	Gln	Leu 140	Ala	Asp	His	Tyr	
Gln 145	Gln	Asn	Thr	Pro	Ile 150	Gly	Asp	Gly	Pro	Val 155	Leu	Leu	Pro	Asp	Asn 160	
His	Tyr	Leu	Ser	Tyr 165	Gln	Ser	Ala	Leu	Ser 170	Lys	Asp	Pro	Asn	Glu 175	Lys	
Arg	Asp	His	Met 180	Val	Leu	Leu	Glu	Phe 185	Val	Thr	Ala	Ala	Gly 190	Ile	Thr	
Leu	Gly	Met 195	Asp	Glu	Leu	Tyr	Lys 200									
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						acc Thr										96
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						cag Gln 55										192
ggc Gly 65	aac Asn	tac Tyr	aag Lys	acc Thr	cgc Arg 70	gcc Ala	gag Glu	gtg Val	aag Lys	ttc Phe 75	gag Glu	ggc Gly	gac Asp	acc Thr	ctg Leu 80	240
						aag Lys										288
						gag Glu										336

	100		105		110	
		Gln Lys A		c aag gcc aac e Lys Ala Asn 125		384
				g ctc gcc gac n Leu Ala Asp 140		432
	Pro Ile			g ctg ctg ccc l Leu Leu Pro 155		480
				a gac ccc aac s Asp Pro Asn 0		528
				c gcc gcc ggg r Ala Ala Gly		576
ggc atg gac Gly Met Asp 195						597
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<220>						
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	E. frag.;	CGFP F2A	., N146I/V	163A/T203Y mut	ations	
<223> modifi <400> 141				163A/T203Y mut r Thr Gly Lys		
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Ile	Met	Ala 115	Asp	Lys	Gln	Lys	Asn 120	Gly	Ile	Lys	Ala	Asn 125	Phe	Lys	Ile	
Arg	His 130	Asn	Ile	Glu	Asp	Gly 135	Ser	Val	Gln	Leu	Ala 140	Asp	His	Tyr	Gln	
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Tyr	Leu	Ser	Tyr	Gln 165	Ser	Ala	Leu	Ser	Lys 170	Asp	Pro	Asn	Glu	Lys 175	Arg	
Asp	His	Met	Val 180	Leu	Leu	Glu	Phe	Val 185	Thr	Ala	Ala	Gly	Ile 190	Thr	Leu	•
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											tac Tyr					96
ttc Phe	gcc Ala	cgc Arg 35	tac Tyr	ccc Pro	gac Asp	cac His	atg Met 40	aag Lys	cgg Arg	cac His	gac Asp	ttc Phe 45	ttc Phe	aag Lys	tcc Ser	144
gcc Ala	atg Met	ccc Pro	gaa Glu	ggc Gly	tac Tyr	gtc Val	cag Gln	gag Glu	cgc Arg	acc Thr	atc Ile	ttc Phe	ttc Phe	aag Lys	gac Asp	192

gac Asp 65																240
ctg Leu																288
aac Asn																336
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Val	Pro	Trp	Pro 20	Thr	Leu	Val	Thr	Thr 25	Phe	Gly	Tyr	Gly	Leu 30	Gln	Cys	
Phe .	Ala	Arg 35	Tyr	Pro	Asp	His	Met 40	Lys	Arg	His	Asp	Phe 45	Phe	Lys	Ser	

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 105 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 150 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 Leu Gly Met Asp Glu Leu Tyr Lys 195 200 <210> 144 <211> 597 <212> DNA <213> Artificial <220> <223> modif. frag.; CGFP F2A, M153T/V163A/T203Y mutations <220> <221> CDS <222> (1)..(597) <400> 144 ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe

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		cgc acc atc ttc Arg Thr Ile Phe 60	
		gtg aag ttc gag Val Lys Phe Glu 75	
		atc gac ttc aag Ile Asp Phe Lys 90	
		aac tac aac agc Asn Tyr Asn Ser 105	
		ggc atc aag gcc Gly Ile Lys Ala	
		gtg cag ctc gcc Val Gln Leu Ala 140	Asp His Tyr Gln
		ccc gtg ctg ctg Pro Val Leu Leu 155	
		agc aaa gac ccc Ser Lys Asp Pro 170	
		gtg acc gcc gcc Val Thr Ala Ala 185	
ggc atg gac gag Gly Met Asp Glu 195			5 <u>9</u> 7
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Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175

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Gly Met Asp Glu Leu Tyr Lys 195

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Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
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ttc gcc cgc tac ccc gac cac atq aaq cqq cac qac ttc ttc aaq tcc
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Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
gec atg ecc gaa gge tac gte cag gag ege acc atc tte tte aag gae
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Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
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gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc
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Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
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Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
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aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
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Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
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Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
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                            120
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac
                                                                      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
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                        135
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac
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Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag
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His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
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ctc c Leu G																600
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Phe A	ala	Arg 35	Tyr	Pro	Asp	His	Met 40	Lys	Arg	His	Asp	Phe 45	Phe	Lys	Ser	
Ala M	let 50	Pro	Glu	Gly	Tyr	Val 55	Gln	Glu	Arg	Thr	Ile 60	Phe	Phe	Lys	Asp	
Asp G 65	Sly	Asn	Tyr	Lys	Thr 70	Arg	Ala	Glu	Val	Lys 75	Phe	Glu	Gly	Asp	Thr 80	
Leu V	al	Asn	Arg	Ile 85	Glu	Leu	Lys	Gly	Ile 90	Asp	Phe	Lys	Glu	Asp 95	Gly	
Asn I	le	Leu	Gly 100	His	Lys	Leu	Glu	Tyr 105	Asn	Tyr	Asn	Ser	His 110	Asn	Val	
Tyr I	le	Thr 115	Ala	Asp	Lys	Gln	Lys 120	Asn	Gly	Ile	Lys	Ala 125	Asn	Phe	Lys	
Ile A	arg .30	His	Asn	Ile	Glu	Asp 135	Gly	Ser	Val	Gln	Leu 140	Ala	Asp	His	Tyr	
Gln G 145	Sln	Asn	Thr	Pro	Ile 150	Gly	Asp	Gly	Pro	Val 155	Leu	Leu	Pro	Asp	Asn 160	

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432

ege cae aac ate gag gae gge age gtg cag ete gee gae cae tae cag

130 135	Leu Ala Asp His Tyr Gln 140
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tac ctg agc tac cag tcc gcc ctg agc aaa Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys 165	Asp Pro Asn Glu Lys Arg
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20 25 Ala Arg Tyr Pro Asp His Met Lys Arg His	30 Asp Phe Phe Lys Ser Ala 45
Ala Arg Tyr Pro Asp His Met Lys Arg His 35 40 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr	30 Asp Phe Phe Lys Ser Ala 45 The Phe Phe Lys Asp Asp 60
Ala Arg Tyr Pro Asp His Met Lys Arg His 40 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr 55 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys	30 Asp Phe Phe Lys Ser Ala 45 Ile Phe Phe Lys Asp Asp 60 Phe Glu Gly Asp Thr Leu 75
Ala Arg Tyr Pro Asp His Met Lys Arg His 40 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr 55 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys 65 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp	30 Asp Phe Phe Lys Ser Ala 45 Ile Phe Phe Lys Asp Asp 60 Phe Glu Gly Asp Thr Leu 75 Phe Lys Glu Asp Gly Asn 95

130	Glu Asp	Gly Ser 135	Val Gln	Leu Ala 140	Asp His	Tyr (Gln
Gln Asn Thr Pro 145	Ile Gly 150		Pro Val	Leu Leu 155	Pro Asp		His 160
Tyr Leu Ser Tyr	Gln Ser 165	Ala Leu	Ser Lys 170	_	Asn Glu	Lys 1	Arg
Asp His Met Val	Leu Leu	Glu Phe	Val Thr 185	Ala Ala	Gly Ile 190	Thr 1	Leu .
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atg ggc aag ctg Met Gly Lys Leu	Thr Leu 5 acc ctc	Lys Phe	Ile Cys 10 acc ttc	Thr Thr	Gly Lys	Leu I 15 cag t	Pro tgc 96
atg ggc aag ctg Met Gly Lys Leu 1 gtg ccc tgg ccc Val Pro Trp Pro	Thr Leu 5 acc ctc Thr Leu ccc gac	Lys Phe gtg acc Val Thr cac atg	Ile Cys 10 acc ttc Thr Phe 25 aag cgg	Thr Thr ggc tac Gly Tyr cac gac	Gly Lys ggc ctg Gly Leu 30 ttc ttc	Leu I 15 cag t Gln (Pro tgc 96 Cys tcc 144
atg ggc aag ctg Met Gly Lys Leu 1 gtg ccc tgg ccc Val Pro Trp Pro 20 ttc gcc cgc tac Phe Ala Arg Tyr	Thr Leu 5 acc ctc Thr Leu ccc gac Pro Asp ggc tac	gtg acc Val Thr cac atg His Met 40	Ile Cys 10 acc ttc Thr Phe 25 aag cgg Lys Arg gag cgc	Thr Thr ggc tac Gly Tyr cac gac His Asp acc atc	ggc ctg Gly Leu 30 ttc ttc Phe Phe 45	Leu I 15 cag t Gln (aag t Lys S	ero tgc 96 Cys tcc 144 Ser gac 192
atg ggc aag ctg Met Gly Lys Leu 1 gtg ccc tgg ccc Val Pro Trp Pro 20 ttc gcc cgc tac Phe Ala Arg Tyr 35 gcc atg ccc gaa Ala Met Pro Glu	Thr Leu acc ctc Thr Leu ccc gac Pro Asp ggc tac Gly Tyr aag acc	gtg acc Val Thr cac atg His Met 40 gtc cag Val Gln 55 cgc gcc	Ile Cys 10 acc ttc Thr Phe 25 aag cgg Lys Arg gag cgc Glu Arg gag gtg	Thr Thr ggc tac Gly Tyr cac gac His Asp acc atc Thr Ile 60 aag ttc	ggc ctg Gly Leu 30 ttc ttc Phe Phe 45 ttc ttc Phe Phe gag ggc	Leu II 15 cag t Gln (aag t Lys S aag Q Lys II gac a Asp T	Pro tgc 96 Cys tcc 144 Ser gac 192 Asp

	ggg cac Gly His 100											336
tat atc acc Tyr Ile Thr 115				s Asn								384
atc cgc cac Ile Arg His 130		Glu										432
cag cag aac Gln Gln Asn 145												480
cac tac ctg His Tyr Leu												528
cgc gat cac Arg Asp His												576
ctc ggc atg Leu Gly Met 195		_		/S								600
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Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95	
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 100 105 110	
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 125	
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140	
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	
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gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45	144
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	192

	50					55					60					
														acc Thr		240
														ggc Gly 95		288
														gtc Val		336
														aag Lys		384
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														aac Asn		480
														aag Lys 175		528
														act Thr		576
		gac Asp 195														597
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30

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys Phe

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

20

50 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 70 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 90 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 105 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 120 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 154 <211> 600 <212> DNA <213> Artificial <220> modif. frag.; BFP (blue) F2A, Y66H mutation and Met added <223> @ posit. 1 <220> <221> CDS <222> (1)..(600) <400> 154 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc cac ggc ctg cag tgc 96

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys 20 25 30

ttc gcc cgc t Phe Ala Arg 3						144
gcc atg ccc of Ala Met Pro 0						192
gac ggc aac t Asp Gly Asn 3				s Phe Glu G		240
ctg gtg aac d Leu Val Asn A						288
aac atc ctg g Asn Ile Leu (ggg cac aag Gly His Lys 100	Leu Glu T	tac aac ta Tyr Asn Ty 105	r Asn Ser H	ac aac gtc is Asn Val 10	336
tat atc atg of Tyr Ile Met A						384
atc cgc cac a Ile Arg His A 130						432
cag cag aac a Gln Gln Asn 1 145				l Leu Leu P		480
cac tac ctg a						528
cgc gat cac a		Leu Glu P			ly Ile Thr	576
ctc ggc atg g Leu Gly Met A 195						600
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Leu Gly Met Asp Glu Leu Tyr Lys

195

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ccc tqq ccc acc ctc qtq acc acc ttc qqc tac qqc ctq caq tqc ttc
                                                                        96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
                                 25
gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc
                                                                       144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
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atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac
                                                                       192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
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                         55
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg
                                                                       240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac
                                                                       288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc tat
                                                                       336
Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val Tyr
            100
                                 105
                                                                       384
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Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
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                             120
cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag
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Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130
                                                                       480
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Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145
                    150
                                         155
tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc
                                                                       528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165
                                     170
                                                         175
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc
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597

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Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val Tyr 100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

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ttc gc Phe Al	c cgc a Arg 35	tac Tyr	ccc Pro	gac Asp	cac His	atg Met 40	aag Lys	cgg Arg	cac His	gac Asp	ttc Phe 45	ttc Phe	aag Lys	tcc Ser	144
gcc at Ala Me 50															192
gac gg Asp Gl 65	c aac y Asn	tac Tyr	aag Lys	acc Thr 70	cgc Arg	gcc Ala	gag Glu	gtg Val	aag Lys 75	ttc Phe	gag Glu	ggc Gly	gac Asp	acc Thr 80	240
ctg gt Leu Va															288
aac at Asn Il															336
tat at Tyr Il															384
atc cg Ile Ar	g His														432

cag cag a Gln Gln A 145			Gly Asp									480
cac tac c His Tyr I												528
cgc gat c Arg Asp H												576
				3								600
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Val Pro I	rp Pro 20	Thr Leu	Val Th	Thr 25	Phe	Gly	Tyr	Gly	Leu 30	Gln	Cys	
Phe Ala A	rg Tyr 5	Pro Asp	His Met	. Lys	Arg	His	Asp	Phe 45	Phe	Lys	Ser	•
Ala Met P	ro Glu	Gly Tyr	Val Gli 55	ı Glu	Arg	Thr	Ile 60	Phe	Phe	Lys	Asp	
Asp Gly A	sn Tyr	Lys Thr 70	Arg Ala	ı Glu	Val	Lys 75	Phe	Glu	Gly	Asp	Thr 80	
Leu Val A	sn Arg	Ile Glu 85	Leu Lys	s Gly	Ile 90	Asp	Phe	Lys	Glu	Asp 95	Gly	
Asn Ile L	eu Gly 100	His Lys	Leu Glı	Tyr 105	Asn	Phe	Asn	Ser	His 110	Asn	Val	
Tyr Ile M	et Ala 15	Asp Lys	Gln Lys		Gly	Ile	Lys	Val 125	Asn	Phe	Lys	

Ile	Arg 130	His	Asn	Ile	Glu	Asp 135	Gly	Ser	Val	Gln	Leu 140	Ala	Asp	His	Tyr	
Gln 145	Gln	Asn	Thr	Pro	Ile 150	Gly	Asp	Gly	Pro	Val 155	Leu	Leu	Pro	Asp	Asn 160	
His	Tyr	Leu	Ser	Tyr 165	Gln	Ser	Ala	Leu	Ser 170	Lys	Asp	Pro	Asn	Glu 175	Lys	
Arg	Asp	His	Met 180	Val	Leu	Leu	Glu	Phe 185	Val	Thr	Ala	Ala	Gly 190	Ile	Thr	
Leu	Gly	Met 195	Asp	Glu	Leu	Tyr	Lys 200									
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											gag Glu					240
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		ccc gtg ctg ctg ccc Pro Val Leu Leu Pro 155	
Tyr Leu Ser Thr G		agc aaa gac ccc aac Ser Lys Asp Pro Asn 170	
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100 105 110
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160
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atc cgc c Ile Arg H												432
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Phe Ala A	arg Tyr 5	Pro Asp	His Met 40	Lys	Arg	His	Asp	Phe 45	Phe	Lys	Ser	
Ala Met F	ro Glu	Gly Tyr	Val Gln 55	Glu	Arg	Thr	Ile 60	Phe	Phe	Lys	Asp	

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	Ile	Arg 130	His	Asn	Ile	Glu	Asp 135	Gly	Ser	Val	Gln	Leu 140	Ala	Asp	His	Tyr	
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	His	Tyr	Leu	Ser	Thr 165	Gln	Ser	Ala	Leu	Ser 170	Lys	Asp	Pro	Asn	Glu 175	Lys	
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Ala	Arg	Tyr 35	Pro	Asp	His	Met	Lys 40	Arg	His	Asp	Phe	Phe 45	Lys	Ser	Ala	
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		tac Tyr														240
		cgc Arg														288
		ggg Gly														336
		gcc Ala 115														384
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		acc Thr														480
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Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val Tyr 100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150155155

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Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly His Gly Leu Gln Cys
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                                25
ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc
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Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
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gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac
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                                                                      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85
aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc
                                                                      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val
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                                 105
tat atc atg qcc qac aag cag aag aac ggc atc aag gtg aac ttc aag
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Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
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atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac
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Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
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                        135
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac
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Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145
                    150
                                         155
                                                             160
cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag
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His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
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432

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Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr

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1 Val	Pro		Pro 20	5 Thr	Leu	Val	Thr	Thr 25	10 Leu	Thr	Tyr	Gly	Val 30	15 Gln	Cys		
1 Val Phe	Pro Ser	Trp	Pro 20 Tyr	5 Thr Pro	Leu Asp	Val His	Thr Met 40	Thr 25 Lys	10 Leu Arg	Thr His	Tyr Asp	Gly Phe 45	Val 30	15 Gln Lys	Cys Ser		
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Val Phe Ala Asp	Pro Ser Met 50	Trp Arg 35	Pro 20 Tyr Glu	Thr Pro Gly Lys	Leu Asp Tyr Thr 70	Val His Val 55	Thr Met 40 Gln	Thr 25 Lys Glu	Leu Arg Arg	Thr His Thr Lys 75.	Tyr Asp Ile 60	Gly Phe 45 Phe Glu	Val 30 Phe Phe	Gln Lys Lys Asp	Cys Ser Asp Thr		

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 175	
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cgc cac aac Arg His Asn 130			Ser V							432
cag aac acc Gln Asn Thr 145										480
tac ctg agc Tyr Leu Ser	tac cag Tyr Gln 165	Ser Ala	ctg a Leu S	egc aaa Ser Lys 170	gac ccc Asp Pro	aac Asn	gag Glu	aag Lys 175	cgc Arg	528
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Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

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Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 55 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 70 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys Val 105 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 120 Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 Leu Gly Met Asp Glu Leu Tyr Lys 200 <210> 174 <211> 597 <212> DNA <213> Artificial <223> modif. frag.; YFP F2A, Y203F mutation <220> <221> CDS <222> (1)..(597) ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48 Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96 Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe

20		25	30
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		ag cgc acc atc ttc t lu Arg Thr Ile Phe F 60	
		ag gtg aag ttc gag g lu Val Lys Phe Glu G 75	
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Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

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Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
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ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc
                                                                      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac
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Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
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gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc
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Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
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ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
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Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
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aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
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Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag
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Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
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                            120
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac
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Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
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cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac
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Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac gag aag
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His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
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                                                        175 .
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Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80	
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95	
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 115 120 125	
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 130 135 140	
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	

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Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln

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Tyr Leu Ser His			c ccc aac gag aag p Pro Asn Glu Lys 175	
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Met Pro Glu Gly 50	Tyr Val Gln 55	Glu Arg Thr Ile	Phe Phe Lys Asp 60	Asp
Gly Asn Tyr Lys	Thr Arg Ala 70	Glu Val Lys Phe 75	e Glu Gly Asp Thr	Leu 80
	Glu Leu Lys 85	Gly Ile Asp Phe	e Lys Glu Asp Gly 95	Asn
Ile Leu Gly His	Lys Leu Glu	Tyr Asn Tyr Asn 105	n Ser His Asn Val 110	Tyr
Ile Met Ala Asp	Lys Gln Lys	Asn Gly Ile Lys	Val Asn Phe Lys	Ile

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln 130 135 140
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160
Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 175
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	Thr Pro 1		ggc ccc gtg Gly Pro Val 155		
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Asn	Ile	Leu	Gly 100	His	Lys	Leu	Glu	Tyr 105	Asn	Tyr	Asn	Ser	His 110	Asn	Val	
Tyr	Ile	Met 115	Ala	Asp	Lys	Gln	Lys 120	Asn	Gly	Ile	Lys	Val 125	Asn	Phe	Lys	
Ile	Arg 130	His	Asn	Ile	Glu	Asp 135	Gly	Ser	Val	Gln	Leu 140	Ala	Asp	His	Tyr	
Gln 145	Gln	Asn	Thr	Pro	Ile 150	Gly	Asp	Gly	Pro	Val 155	Leu	Leu	Pro	Asp	Asn 160	
His	Tyr	Leu	Ser	His 165	Gln	Ser	Ala	Leu	Ser 170	Lys	Asp	Pro	Asn	Glu 175	Lys	
Arg	Asp	His	Met 180	Val	Leu	Leu	Glu	Phe 185	Val	Thr	Ala	Ala	Gly 190	Ile	Thr	
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					acc Thr 70											240
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		_	_		aag Lys							_			_	336
					aag Lys											384
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Phe	Ala	Arg 35	Tyr	Pro	Asp	His	Met 40	Lys	Arg	His	Asp	Phe 45	Phe	Lys	Ser	

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ggc aac tac aag acc cgc gcc Gly Asn Tyr Lys Thr Arg Ala 65 70		
gtg aac cgc atc gag ctg aag Val Asn Arg Ile Glu Leu Lys 85		
atc ctg ggg cac aag ctg gag Ile Leu Gly His Lys Leu Glu 100		
atc atg gcc gac aag cag aag Ile Met Ala Asp Lys Gln Lys 115		n Phe Lys Ile
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cag aac acc ccc atc ggc gac Gln Asn Thr Pro Ile Gly Asp 145 150		
tac ctg agc tac cag tcc gcc Tyr Leu Ser Tyr Gln Ser Ala 165		
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Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 110

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
115 · 120 125

Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

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Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

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                                                                       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
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ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc
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Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
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Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
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aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
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Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
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tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag
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Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
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ate ege cac aac ate gag gae gge gge gtg cag ete gee gae cac tac
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Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr
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                        135
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Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
cac tac ctg age tac cag tcc gcc ctg age aaa gac ccc aac gag aag
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His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
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432

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Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln

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		ctg agc aaa gac Leu Ser Lys Asp 170	Pro Asn Glu L	
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ggc atg gac gag Gly Met Asp Glu 195				597
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Val Asn Arg Ile	Glu Leu Lys 85	Gly Ile Asp Phe	Lys Glu Asp G 9	-
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Ile Thr Ala Asp	Lys Gln Lys	Asn Gly Ile Lys	Val Asn Phe L	ys Ile

Arg	His 130	Asn	Ile	Glu	Asp	Gly 135	Gly	Val	Gln	Leu	Ala 140	Asp	His	Tyr	Gln	
Gln 145	Asn	Thr	Pro	Ile	Gly 150	Asp	Gly	Pro	Val	Leu 155	Leu	Pro	Asp	Asn	His 160	
Tyr	Leu	Ser	Tyr	Gln 165	Ser	Ala	Leu	Ser	Lys 170	Asp	Pro	Asn	Glu	Lys 175	Arg	
Asp	His	Met	Val 180	Leu	Leu	Glu	Phe	Val 185	Thr	Ala	Ala	Gly	Ile 190	Thr	Leu	
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		tgg Trp														96
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Phe		Arg 35									gac Asp					-
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Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val

Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe I 115 120 125	aag 384 .ys
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cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac ac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Ap 145	
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag a His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu I 165 170 175	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc a Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile T 180 185 190	
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 195 200	600
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<223> modif.frag.; Venus F2A, M153T, S175G mutations and Met	
<223> modif.frag.; Venus F2A, M153T, S175G mutations and Metadded @ posit. 1	
<223> modif.frag.; Venus F2A, M153T, S175G mutations and Met added @ posit. 1 <400> 191	Pro
<pre><223> modif.frag.; Venus F2A, M153T, S175G mutations and Met added @ posit. 1 <400> 191 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu F 1</pre>	Pro Pro
<pre><223> modif.frag.; Venus F2A, M153T, S175G mutations and Met added @ posit. 1 <400> 191 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu F 1</pre>	ro 'ys er
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Asn Ile Leu G	Gly His	Lys Leu	Glu Tyr 10	_	Asn Ser	His Asn 110	Val
Tyr Ile Thr A	Ala Asp	Lys Gln	Lys Ası 120	n Gly Ile	Lys Val	Asn Phe	Lys
Ile Arg His A	Asn Ile	Glu Asp 135	Gly Gly	√ Val Gln	Leu Ala 140	Asp His	Tyr
Gln Gln Asn T 145	Thr Pro	Ile Gly 150	Asp Gly	Pro Val 155		Pro Asp	Asn 160
His Tyr Leu S	Ser Tyr 165	Gln Ser	Ala Le	Ser Lys 170	Asp Pro	Asn Glu 175	Lys
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Leu Gly Met A	Asp Glu	Leu Tyr	Lys 200				
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atg ccc gaa g Met Pro Glu G 50							
ggc aac tac a							

65	70	75	80
		ttc aag gag gac ggc Phe Lys Glu Asp Gly 95	
		aac agc cac aac gtc Asn Ser His Asn Val	
		aag gcc aac ttc aag Lys Ala Asn Phe Lys 125	
		ctc gcc gac cac tac Leu Ala Asp His Tyr	
		ctg ctg ccc gac aac Leu Leu Pro Asp Asn 155	
	Ser Ala Leu Ser Lys	gac ccc aac gag aag Asp Pro Asn Glu Lys 175	
		gcc gcc ggg atc act Ala Ala Gly Ile Thr 190	
ggc atg gac gag ctg Gly Met Asp Glu Leu 195			597
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Pro Trp Pro Thr Leu 20	Val Thr Thr Phe Gly 25	Tyr Gly Leu Gln Cys 30	Phe
Ala Arg Tyr Pro Asp 35	His Met Lys Arg His	Asp Phe Phe Lys Ser 45	Ala
Met Pro Glu Gly Tyr 50	Val Gln Glu Arg Thr	Ile Phe Phe Lys Asp	Asp

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 90 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 105 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 120 Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln 130 135 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 Gly Met Asp Glu Leu Tyr Lys 195 <210> 194 <211> 600 <212> DNA <213> Artificial <220> modif. frag.; Venus F2A, w. V163A, S175G mutations and Met added @ posit. 1 <220> <221> CDS <222> (1)..(600)<400> 194 atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48 Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96 Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys 25 ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144 Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45

					tac Tyr											192
					acc Thr 70											240
					gag Glu											288
aac Asn	atc Ile	ctg Leu	ggg Gly 100	cac His	aag Lys	ctg Leu	gag Glu	tac Tyr 105	aac Asn	tac Tyr	aac Asn	agc Ser	cac His 110	aac Asn	gtc Val	336
					aag Lys											384
					gag Glu											432
					atc Ile 150											480
					cag Gln											528
					ctg Leu											576
					ctg Leu											600
<210 <211 <212 <213	L> 2 2> E	195 200 PRT Artif	icia	al												
<220 <220	3> n				Ver			w. \	/163/	A, S1	L75G	muta	ation	ıs		
<400)> 1	95														
Met 1	Gly	Lys	Leu	Thr 5	Leu	Lys	Phe	Ile	Cys 10	Thr	Thr	Gly	Lys	Leu 15	Pro	
Val	Pro	Trp	Pro 20	Thr	Leu	Val	Thr	Thr 25	Phe	Gly	Tyr	Gly	Leu 30	Gln	Cys	

Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 40 Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 75 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 100 105 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr 130 135 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 150 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 165 170 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 190 Leu Gly Met Asp Glu Leu Tyr Lys 195 <210> 196 <211> 597 <212> DNA <213> Artificial <220> <223> modif. frag.; Venus F2A,F46L/F64L/M153T/V163A/S175G mutations <220> <221> CDS <222> (1)..(597) ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc gtg

Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val

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	ctc gtg acc acc ctc Leu Val Thr Thr Leu 25		
	gac cac atg aag cgg Asp His Met Lys Arg 40		
	tac gtc cag gag cgc Tyr Val Gln Glu Arg 55		
	acc cgc gcc gag gtg Thr Arg Ala Glu Val 70		
	gag ctg aag ggc atc Glu Leu Lys Gly Ile 85		
	aag ctg gag tac aac Lys Leu Glu Tyr Asn 105		
	aag cag aag aac ggc Lys Gln Lys Asn Gly 120		
	gag gac ggc ggc gtg Glu Asp Gly Gly Val 135		
	atc ggc gac ggc ccc Ile Gly Asp Gly Pro 150		
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	ctg ctg gag ttc gtg Leu Leu Glu Phe Val 185		
ggc atg gac gag Gly Met Asp Glu 195			597
<210> 197 <211> 199 <212> PRT <213> Artificia	al	·	
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Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe 20 25 30

Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala 35 40 45

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp 50 55 60

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu 65 70 75 80

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn 85 90 95

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr 100 105 110

Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile 115 120 125

Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln 130 135 140

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His 145 150 155 160

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg 165 170 . 175

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu 180 185 190

Gly Met Asp Glu Leu Tyr Lys 195

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		tgg Trp														96
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		ccc Pro														192
		aac Asn														240
		aac Asn														288
		ctg Leu		His		Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn		336
tat Tyr	atc Ile	acc Thr 115	gcc Ala	gac Asp	aag Lys	cag Gln	aag Lys 120	aac Asn	ggc Gly	atc Ile	aag Lys	gcc Ala 125	aac Asn	ttc Phe	aag Lys	384
Ile		cac His								Gln						432
cag Gln 145	cag Gln	aac Asn	acc Thr	ccc Pro	atc Ile 150	ggc Gly	gac Asp	ggc Gly	ccc Pro	gtg Val 155	ctg Leu	ctg Leu	ccc Pro	gac Asp	aac Asn 160	480
		ctg Leu														528

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 180 185 190	576
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 195 200	600
<210> 199 <211> 200 <212> PRT <213> Artificial	
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Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys 20 25 30	
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser 35 40 45	
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 50 55 60	
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 65 70 75 80	
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 85 90 95	
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val	
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 115 120 125	
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr 130 135 140	
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 145 150 155 160	

165 170 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 185 190 Leu Gly Met Asp Glu Leu Tyr Lys 195 <210> 200 <211> 306 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F1B (aa residues 1-103 of YFP) with posit. 1 Met removed <220> <221> CDS <222> (1)..(306) <400> 200 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 48 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 25 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 4.0 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 55 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240 . Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 acc atc ttc ttc aag gac 306 Thr Ile Phe Phe Lys Asp 100

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys

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<213> Artificial
<220>
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                                  10
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
                               25
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                           40
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
                       55
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
                  70
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
               85
                                   90
Thr Ile Phe Phe Lys Asp
           100
<210> 202
<211> 309
<212> DNA
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Τ,
      residue 69 is V, and residue 73 is S
<220>
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<400> 202
atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg
                                                                     48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
               5
                                   10
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Val Glu Leu As	sp Gly Asp		y His Lys		gtg tcc ggc Val Ser Gly 30	96
gag ggc gag gg Glu Gly Glu G: 35						144
tgc acc acc gg Cys Thr Thr G			o Trp Pro			192
ctc acc tac go Leu Thr Tyr G 65						240
cgg cac gac tt Arg His Asp Ph						288
cgc acc atc to Arg Thr Ile Ph 10						309
<210> 203 <211> 103 <212> PRT <213> Artific	cial					
Т,	_			idue 65	is L, residue 66	is
<223> modif. T, residue	_	P F1B, amin		idue 65	is L, residue 66	is
<223> modif. T, residue <400> 203	e 69 is V,	and residu	e 73 is S			is
<223> modif. T, residue	e 69 is V,	and residu	e 73 is S			is
<pre><223> modif. T,</pre>	e 69 is V, vs Gly Glu 5	and residu	e 73 is S Thr Gly 10 y His Lys	Val Val	Pro Ile Leu 15	is
<pre><223> modif. T,</pre>	e 69 is V, vs Gly Glu 5 sp Gly Asp	and residu Glu Leu Ph Val Asn Gl	e 73 is S e Thr Gly 10 y His Lys	Val Val Phe Ser	Pro Ile Leu 15 Val Ser Gly 30	is
<pre><223> modif. T,</pre>	e 69 is V, ys Gly Glu 5 sp Gly Asp)	and residu Glu Leu Ph Val Asn Gl 25 Thr Tyr Gl 40	e 73 is S e Thr Gly 10 y His Lys y Lys Leu	Val Val Phe Ser Thr Leu 45	Pro Ile Leu 15 Val Ser Gly 30 Lys Phe Ile	is
<pre><223> modif. T,</pre>	e 69 is V, ys Gly Glu 5 sp Gly Asp ly Asp Ala	and residu Glu Leu Ph Val Asn Gl 25 Thr Tyr Gl 40 Pro Val Pr 55	e 73 is S e Thr Gly 10 y His Lys y Lys Leu o Trp Pro	Val Val Phe Ser Thr Leu 45 Thr Leu 60	Pro Ile Leu 15 Val Ser Gly 30 Lys Phe Ile Val Thr Thr	is

Arg Thr Ile Phe Phe Lys Asp

<210> 204 <211> 306 <212> DNA <213> Artificial	
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<220> <221> CDS <222> (1)(306)	
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gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag9Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu253030	96
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	4
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 55 60	}2
acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cgg Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg 70 75 80	ŧ O
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	}8
acc atc ttc ttc aag gac Thr Ile Phe Phe Lys Asp 100)6

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<210> 205
 <211> 102
 <212> PRT
 <213> Artificial
 <220>
 <223> modif. frag. EGFP F1B, amino acid residue 65 is L, residue 66 is
       residue 69 is V, residue 73 is S, and posit. 1 Met has been
 removed
 <400> 205
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                5
                                    10
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                            40
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50
                        55
 Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
                    70
                                        75
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85
Thr Ile Phe Phe Lys Asp
            100
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 <211> 309
<212> DNA
<213> Artificial
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<220>
<221> CDS
<222> (1)..(309)
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                                                                      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
                5
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
                                                                       96
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

		20					25					30			
gag ggc Glu Gly															144
tgc acc Cys Thr 50															192
ttc ggc Phe Gly 65															240
cgg cac Arg His															288
cgc acc Arg Thr															309
<211> <212>	207 103 PRT Arti	ficia	al												
<220> <223>	modi	f. f	rag.	; YI	FP F1	LB wi	ith F	(79R	muta	ation	n				
<400>	207														
Met Val 1	Ser	Lys	Gly 5	Glu	Glu	Leu	Phe	Thr 10	Gly	Val	Val	Pro	Ile 15	Leu	
Val Glu	Leu	Asp 20	Gly	Asp	Val	Asn	Gly 25	His	Lys	Phe	Ser	Val 30	Ser	Gly	
Glu Gly	Glu 35	Gly	Asp	Ala	Thr	Tyr 40	Gly	Lys	Leu	Thr	Leu 45	Lys	Phe	Ile	
Cys Thr 50	Thr	Gly	Lys	Leu	Pro 55	Val	Pro	Trp	Pro	Thr 60	Leu	Val	Thr	Thr	
Phe Gly 65	Tyr	Gly	Leu	Gln 70	Cys	Phe	Ala	Arg	Tyr 75	Pro	Asp	His	Met	Arg 80	
Arg His	Asp	Phe	Phe 85	Lys	Ser	Ala	Met	Pro 90	Glu	Gly	Tyr	Val	Gln 95	Glu	

Arg Thr Ile Phe Phe Lys Asp 100

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<210> 208
<211>
      306
<212> DNA
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       posit. 1 Met removed
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<400> 208
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
                                                                      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
                                                                      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20
                                25
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
                                                                     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                            40
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc
                                                                     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg
                                                                     240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
                                                                     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85
                                    90
acc atc ttc ttc aag gac
                                                                     306
Thr Ile Phe Phe Lys Asp
            100
<210> 209
<211> 102
<212> PRT
<213> Artificial
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      modif. frag.; YFP F1B with K79R mutation and
       posit. 1 Met removed
<400> 209
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                5
                                    10
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu

Gly	Glu	Gly 35	Asp	Ala	Thr	Tyr	Gly 40	Lys	Leu	Thr	Leu	Lys 45	Phe	Ile	Cys	
Thr	Thr 50	Gly	Lys	Leu	Pro	Val 55	Pro	Trp	Pro	Thr	Leu 60	Val	Thr	Thr	Phe	
Gly 65	Tyr	Gly	Leu	Gln	Cys 70	Phe	Ala	Arg	Tyr	Pro 75	Asp	His	Met	Arg	Arg 80	
His	Asp	Phe	Phe	Lys 85	Ser	Ala	Met	Pro	Glu 90	Gly	Tyr	Val	Gln	Glu 95	Arg	
Thr	Ile	Phe	Phe 100	Lys	Asp											
			ficia	al												
<22 <22		nodi	E. fi	rag.	; YI	FP F	lB w	ith Y	766F	mut	ation	ı				
<22 <22 <22	1> (CDS (1).	. (309	9)												
	gtg				gag Glu											48
					gac Asp											96
gag Glu	ggc Gly	gag Glu 35	ggc Gly	gat Asp	gcc Ala	acc Thr	tac Tyr 40	ggc Gly	aag Lys	ctg Leu	acc Thr	ctg Leu 45	aag Lys	ttc Phe	atc Ile	1,44
					ctg Leu											·192
					cag Gln 70											240
					aag Lys											288

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Arg Thr Ile Phe Phe Lys Asp
            100
<210> 211
<211>
      103
<212>
      PRT
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<220>
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                25
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                            40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
                       55
Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
               85
                                    90
Arg Thr Ile Phe Phe Lys Asp
           100
<210> 212
<211> 306
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      posit. 1 Met removed
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<222> (1)..(306)
<400> 212
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
                                                                      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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cgc acc atc ttc ttc aag gac

309

1	5	10		15
gag ctg gac ggc Glu Leu Asp Gly 20				
ggc gag ggc gat Gly Glu Gly Asp 35	Ala Thr Tyr G			
acc acc ggc aag Thr Thr Gly Lys 50				
ggc ttc ggc ctg Gly Phe Gly Leu 65		Ala Arg Tyr P		
cac gac ttc ttc His Asp Phe Phe				
acc atc ttc ttc Thr Ile Phe Phe 100				306
<210> 213 <211> 102 <212> PRT <213> Artificia	al			
	rag.; YFP F1B Met removed	with Y66F m	nutation and	
<400> 213				
<400> 213 Val Ser Lys Gly 1	Glu Glu Leu P 5	Phe Thr Gly V 10	al Val Pro Ile	Leu Val 15
Val Ser Lys Gly	5	10		15
Val Ser Lys Gly 1 Glu Leu Asp Gly	5 Asp Val Asn G Ala Thr Tyr G	10 Ely His Lys P 25	Phe Ser Val Ser 30	15 Gly Glu
Val Ser Lys Gly Glu Leu Asp Gly 20 Gly Glu Gly Asp	5 Asp Val Asn G Ala Thr Tyr G 4	10 Gly His Lys P 25 Gly Lys Leu T	The Ser Val Ser 30 Thr Leu Lys Phe 45	Gly Glu Ile Cys
Val Ser Lys Gly Glu Leu Asp Gly 20 Gly Glu Gly Asp 35 Thr Thr Gly Lys	Asp Val Asn G Ala Thr Tyr G 4 Leu Pro Val P 55	IO Gly His Lys P 25 Gly Lys Leu T 10 Pro Trp Pro T	The Ser Val Ser 30 Thr Leu Lys Phe 45 Thr Leu Val Thr 60	Gly Glu Ile Cys Thr Phe

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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
                                                                     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                            40
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag
                                                                     240
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                    70
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
                                                                     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
cgc acc atc ttc ttc aag gac
                                                                     309
Arg Thr Ile Phe Phe Lys Asp
           100
<210> 215
<211> 103
<212> PRT
<213> Artificial
<223> modif. frag.; YFP F1B with Q69K mutation
<400> 215
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Thr Ile Phe Phe Lys Asp

10

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 25 20 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 40 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 55 Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys 70 75 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 100 <210> 216 <211> 306 <212> DNA <213> Artificial <220> modif. frag.; YFP F1B with Q69K mutation and <223> posit. 1 Met removed <220> <221> CDS <222> (1)..(306)<400> 216 gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg gtc . 48 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 25 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 40 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 55 60 ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240 Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 306 acc atc ttc ttc aag gac Thr Ile Phe Phe Lys Asp 100 <210> 217 <211> 102 <212> PRT <213> Artificial <220> <223> modif. frag.; YFP F1B with Q69K mutation and posit. 1 Met removed <400> 217 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 5 10 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 . 70 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85

Thr Ile Phe Phe Lys Asp 100

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       309
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
                                                                       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                25
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
                                                                      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
tte gge tae gge etg eag tge tte gee ege tae eee gae eae atg ege
                                                                      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
65
                    70
egg cac gac ttc ttc aag tee gee atg eee gaa gge tae gte eag gag
                                                                      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85
cgc acc atc ttc ttc aag gac
                                                                      309
Arg Thr Ile Phe Phe Lys Asp
            100
<210> 219
<211> 103
<212>
      PRT
<213> Artificial
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      modif. frag.; YFP F1B with K79R mutation
<223>
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      219
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
                5
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                25
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 40 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 Arg Thr Ile Phe Phe Lys Asp 100 <210> 220 <211> 306 <212> DNA <213> Artificial <220> modif. frag.; YFP F1B with K79R mutation and <223> posit. 1 Met removed <220> <221> CDS <222> (1)..(306)<400> 220 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg 240 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90

306

acc atc ttc ttc aag gac

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Thr Ile Phe Phe Lys Asp
100
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<210> 221

<211> 102

<212> PRT

<213> Artificial

<220>

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<400> 221

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5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

Thr Ile Phe Phe Lys Asp 100

<210> 222

<211> 309

<212> DNA

<213> Artificial

<220s

<223> modif. frag.; citrine F1B, with V68L, Q69M mutations

<220>

<221> CDS

<222> (1)..(309)

<400> 222

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15 48

val Glu Leu	gac ggc Asp Gly 20		Asn								,96
gag ggc gag Glu Gly Glu 35											144
tgc acc acc Cys Thr Thr 50											192
ttc ggc tac Phe Gly Tyr 65											240
cgg cac gac Arg His Asp					o Glu						288
cgc acc atc Arg Thr Ile											309
<210> 223 <211> 103 <212> PRT <213> Arti:	ficial					,					
<220>											
	f. frag.;	citrin	e F1B	, with	V681	٠. ٥٥	59M n	nıtat	ione	,	
						. ~				•	
<400> 223										•	
<pre><400> 223 Met Val Ser 1</pre>	Lys Gly 5	Glu Glu	Leu		r Gly						
Met Val Ser	5		Asn (Phe Th	r Gly	Val	Val	Pro	Ile 15	Leu	
Met Val Ser 1	5 Asp Gly 20	Asp Val	Asn (Phe Th 10 Gly Hi 25	r Gly s Lys	Val Phe	Val Ser	Pro Val 30	Ile 15 Ser	Leu Gly	
Met Val Ser 1 Val Glu Leu Glu Gly Glu	Asp Gly 20 Gly Asp	Asp Val	Asn (Phe Th 10 Gly Hi 25 Gly Ly	r Gly s Lys s Leu	Val Phe Thr	Val Ser Leu 45	Pro Val 30 Lys	Ile 15 Ser	Leu Gly Ile	
Met Val Ser 1 Val Glu Leu Glu Gly Glu 35 Cys Thr Thr	Asp Gly 20 Gly Asp	Asp Val Ala Thr Leu Pro 55	Asn (Tyr (40)	Phe Th 10 Gly Hi 25 Gly Ly Pro Tr	s Lys s Leu	Val Phe Thr	Val Ser Leu 45	Pro Val 30 Lys Val	Ile 15 Ser Phe	Leu Gly Ile Thr	

Arg Thr Ile Phe Phe Lys Asp

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<210> 224
<211>
      306
<212>
      DNA
<213>
      Artificial
<220>
<223>
      modif. frag.; citrine F1B, with V68L, Q69M mutations
       and posit. 1 Met removed
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<221> CDS
<222> (1)..(306)
<400> 224
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                                                                      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
                                                                      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
                                25
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
                                                                     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                            40
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc
                                                                     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
                        55
ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg
                                                                     240
Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
                                                                     288
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
               85
                                    90
acc atc ttc ttc aag gac
                                                                     306
Thr Ile Phe Phe Lys Asp
            100
<210> 225
<211> 102
<212> PRT
<213> Artificial
<220>
      modif. frag.; citrine F1B, with V68L, Q69M mutations
      and posit. 1 Met removed
<400> 225
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                5
                                    10
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 40 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 Thr Ile Phe Phe Lys Asp 100 <210> 226 <211> 309 <212> DNA <213> Artificial <220> <223> modif. frag.; Venus F1B with F46L, F64L mutations <220> <221> CDS <222> (1)..(309) <400> 226 atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 egg cae gae the the aag tee gee and eee gaa gge tae gte eag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu

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Arg Thr Ile Phe Phe Lys Asp
            100
<210> 227
<211> 103
<212> PRT
<213> Artificial
<220>
<223> modif. fraq.; Venus F1B with F46L, F64L mutations
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
                5
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                25
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
                            40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
                       55
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                   70
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
             85
                                    90
Arg Thr Ile Phe Phe Lys Asp
            100
<210> 228
<211> 306
<212> DNA
<213> Artificial
<220>
<223> modif. frag.; Venus F1B with F46L, F64L mutations
       and posit. 1 Met removed
<220>
<221> CDS
<222> (1)..(306)
<400> 228
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
                                                                      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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309

cgc acc atc ttc ttc aag gac

1	5	10	15
	gac gta aac ggc cac Asp Val Asn Gly His 25		
	gcc acc tac ggc aag Ala Thr Tyr Gly Lys 40		
	ctg ccc gtg ccc tgg Leu Pro Val Pro Trp 55		
	cag tgc ttc gcc cgc Gln Cys Phe Ala Arg 70		
	aag tcc gcc atg ccc Lys Ser Ala Met Pro 85		
acc atc ttc ttc Thr Ile Phe Phe 100			306
<210> 229 <211> 102 <212> PRT <213> Artificia	al		
	rag.; Venus F1B with t. 1 Met removed	F46L, F64L mutations	3
<400> 229			
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Glu Leu Asp Gly 20	Asp Val Asn Gly His 25	Lys Phe Ser Val Ser	Gly Glu
Gly Glu Gly Asp 35	Ala Thr Tyr Gly Lys	Leu Thr Leu Lys Leu 45	Ile Cys
		43	
Thr Thr Gly Lys	Leu Pro Val Pro Trp 55		Thr Leu
50	-	Pro Thr Leu Val Thr 60	

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<210> 230
<211>
      309
<212> DNA
<213>
      Artificial
<220>
<223> modif. frag.; YFP F1B with F46L mutation
<220>
<221> CDS
<222> (1)..(309)
<400> 230
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
                                                                      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
gto gag otg gac ggo gac gta aac ggo cac aag tto ago gtg too ggo
                                                                      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                25
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc
                                                                     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
tte gge tac gge etg eag tge tte gee ege tac eec gae eac atg aag
                                                                     240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag
                                                                     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                                    90
cgc acc atc ttc ttc aag gac
                                                                     309
Arg Thr Ile Phe Phe Lys Asp
            100
<210> 231
<211> 103
<212> PRT
<213> Artificial
<220>
      modif. frag.; YFP F1B with F46L mutation
<400> 231
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Thr Ile Phe Phe Lys Asp

	20	Asp Val	Asn Gly 25	His Lys	Phe Ser	Val 30	Ser	Gly	·
Glu Gly Glu 35	Gly Asp	Ala Thr	Tyr Gly 40	Lys Leu	Thr Leu 45	Lys	Leu	Ile	
Cys Thr Thr 50	Gly Lys	Leu Pro 55	Val Pro	Trp Pro	Thr Leu 60	Val	Thr	Thr	
Phe Gly Tyr 65		Gln Cys 70	Phe Ala	Arg Tyr 75	Pro Asp	His	Met	Lys 80	
Arg His Asp	Phe Phe 85	Lys Ser	Ala Met	Pro Glu 90	Gly Tyr	Val	Gln 95	Glu	
Arg Thr Ile	Phe Phe	Lys Asp							
<210> 232 <211> 306 <212> DNA <213> Arti	ficial								
	f. frag.; t. 1 Met		.B with 1	F46L muta	ation an	ıd			
<223> modi posi <220> <221> CDS			B with D	₹46L muta	ation ar	ıd			
<223> modi posi <220> <221> CDS	t. 1 Met .(306)	removed	ttc acc	ggg gtg	gtg ccc	atc			48
<223> modi posi <220> <221> CDS <222> (1). <400> 232 gtg agc aag Val Ser Lys	.(306) ggc gag Gly Glu 5 ggc gac	removed gag ctg Glu Leu gta aac	ttc acc Phe Thr ggc cac	ggg gtg Gly Val 10 aag ttc	gtg ccc Val Pro	atc Ile	Leu 15 ggc	Val gag	48
<223> modi posi <220> <221> CDS <222> (1). <400> 232 gtg agc aag Val Ser Lys 1 gag ctg gac	d. 1 Met (306) ggc gag gly Gly Gly Gly Asp 20 gat gcc gat gcc	gag ctg Glu Leu gta aac Val Asn	ttc acc Phe Thr ggc cac Gly His 25 ggc aag	ggg gtg Gly Val 10 aag ttc Lys Phe	gtg ccc Val Pro agc gtg Ser Val	atc Ile tcc Ser 30	Leu 15 ggc Gly atc	Val gag Glu tgc	
<223> modi posi <220> <221> CDS <222> (1). <400> 232 gtg agc aag Val Ser Lys 1 gag ctg gac Glu Leu Asp ggc gag ggc Gly Glu Gly	d. 1 Met .(306) ggc gag Gly Glu 5 ggc gac Gly Asp 20 gat gcc Asp Ala	gag ctg Glu Leu gta aac Val Asn acc tac Thr Tyr	ttc acc Phe Thr ggc cac Gly His 25 ggc aag Gly Lys 40 ccc tgg	ggg gtg Gly Val 10 aag ttc Lys Phe ctg acc Leu Thr	gtg ccc Val Pro agc gtg Ser Val ctg aag Leu Lys 45	atc Ile tcc Ser 30 ctg Leu	Leu 15 ggc Gly atc Ile	yal gag Glu tgc Cys	96

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 acc atc ttc ttc aag gac 306 Thr Ile Phe Phe Lys Asp 100 <210> 233 <211> 102 <212> PRT <213> Artificial <220> <223> modif. frag.; YFP F1B with F46L mutation and posit. 1 Met removed <400> 233 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys 35 40 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 70 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90

Thr Ile Phe Phe Lys Asp 100

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<210> 234
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 <212> DNA
 <213>
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 <220>
       modif. frag.; CFP F1B with F64L mutation
 <223>
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       CDS
 <222>
        (1)..(309)
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atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
                                                                        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
                                     10
                                                                        .96
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                 25
             20
                                                                       144
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                             40
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50
                         55
ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
                                                                       240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                    .70
egg cae gae tte tte aag tee gee atg eee gaa gge tae gte cag gag
                                                                       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                 85
                                     90
cgc acc atc ttc ttc aag gac
                                                                       309
Arq Thr Ile Phe Phe Lys Asp
             100
 <210> 235
<211>
       103
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       PRT
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 <220>
       modif. frag.; CFP F1B with F64L mutation
 <223>
 <400>
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
                 5
                                                          15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 55 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 90 Arg Thr Ile Phe Phe Lys Asp 100 <210> 236 <211> 306 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F1B with F64L mutation and posit. 1 Met removed <220> <221> CDS <222> (1)..(306) <400> 236 gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg gtc 48 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 acc atc ttc ttc aag gac 306

Thr Ile Phe Phe Lys Asp

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      102
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<212>
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
                               25
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                           40
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
                   70
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
               85
                   90
Thr Ile Phe Phe Lys Asp
           100
<210> 238
<211> 309
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<220>
<221>
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<222> (1)..(309)
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                                                                     48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
                                                                     96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
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20 25 30

Glu Gly Glu G 35	gc gat gcc ly Asp Ala						
tgc acc acc g Cys Thr Thr G 50							
ttc ggc tgg gg Phe Gly Trp G 65						Met :	
cgg cac gac t Arg His Asp P	tc ttc aag he Phe Lys 85	tcc gcc Ser Ala	atg ccc Met Pro 90	gaa ggc Glu Gly	tac gtc Tyr Val	cag (Gln (95	gag 288 Glu
cgc acc atc t Arg Thr Ile P	_	_					309
<210> 239 <211> 103 <212> PRT <213> Artific	cial						<u>-</u>
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Met Val Ser L	5 sp Gly Asp		10	-		15	
Met Val Ser L	5 sp Gly Asp 0	Val Asn	10 Gly His 25	Lys Phe	Ser Val	15 Ser (Gly
Met Val Ser Ly Val Glu Leu A Glu Gly Glu G	5 sp Gly Asp 0 ly Asp Ala	Val Asn Thr Tyr 40	Gly His 25 Gly Lys	Lys Phe	Ser Val 30 Leu Lys 45	Ser (Gly Ile
Met Val Ser Ly Val Glu Leu Ag Glu Gly Glu G 35 Cys Thr Thr G	5 sp Gly Asp 0 ly Asp Ala ly Lys Leu	Val Asn Thr Tyr 40 Pro Val 55	Gly His 25 Gly Lys Pro Trp	Lys Phe Leu Thr Pro Thr 60	Ser Val 30 Leu Lys 45	Ser (Gly Ile Thr
Met Val Ser Ly Val Glu Leu Ag Glu Gly Glu G 35 Cys Thr Thr G 50 Phe Gly Trp G	sp Gly Asp 0 ly Asp Ala ly Lys Leu ly Leu Gln 70	Val Asn Thr Tyr 40 Pro Val 55 Cys Phe	Gly His 25 Gly Lys Pro Trp Ala Arg	Lys Phe Leu Thr Pro Thr 60 Tyr Pro 75	Ser Val 30 Leu Lys 45 Leu Val	Ser (Gly Ile Thr Lys 30

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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                                    10
                                                                       96
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
                                25
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
                                                                      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                            40
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc
                                                                      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50
                        55
ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg
                                                                      240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65
                    70
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
                                                                      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85
                                                                      306
acc atc ttc ttc aag gac
Thr Ile Phe Phe Lys Asp
            100
<210> 241
<211> 102
      PRT
<212>
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                5
                                    10
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20
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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 40 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 55 Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 100 <210> 242 <211> 309 <212> DNA <213> Artificial <223> modif. frag.; CFP F1B with S65A mutation <220> <221> CDS <222> (1)..(309) <400> 242 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 tte gee tae gge etg cag tge tte gee ege tae eee gae cae atg aag 240 Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu cgc acc atc ttc ttc aag gac 309

Arg Thr Ile Phe Phe Lys Asp

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       103
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                                    10
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                 25
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                             40
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                    70
                                         75
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85
Arg Thr Ile Phe Phe Lys Asp
<210> 244
<211> 306
<212> DNA
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       modif. frag.; CFP F1B with S65A mutation and posit. 1 Met removed
<223>
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       CDS
<221>
<222> (1)..(306)
<400> 244
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
                                                                       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
                                                                       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
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20 25 30

35			aag ctg acc Lys Leu Thr			
acc acc ggc as Thr Thr Gly Ly 50						
gcc tac ggc ct Ala Tyr Gly Le 65						
cac gac ttc tt His Asp Phe Ph						
acc atc ttc tt Thr Ile Phe Ph 10	ne Lys Asp					306
<210> 245 <211> 102 <212> PRT <213> Artific	cial					
<220> <223> modif.	frag.; CFI	P F1B with	h S65A muta	tion and	posit. 1	l Met removed
	frag.; CFI	P F1B with	h S65A muta	ition and	posit. 1	Met removed
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<223> modif. <400> 245 Val Ser Lys Gl	ly Glu Glu 5 ly Asp Val	Leu Phe T	Thr Gly Val	. Val Pro	Ile Leu 15	Val
<223> modif. <400> 245 Val Ser Lys Gl 1 Glu Leu Asp Gl	ly Glu Glu 5 ly Asp Val	Leu Phe T Asn Gly F	Thr Gly Val 10 His Lys Phe 25	Val Pro	Ile Leu 15 Ser Gly 30	Val
<223> modif. <400> 245 Val Ser Lys Gl 1 Glu Leu Asp Gl 20 Gly Glu Gly As	ly Glu Glu 5 ly Asp Val)	Leu Phe TANGLY FOR TYPE Gly IA	Thr Gly Val 10 His Lys Phe 25 Lys Leu Thr	Val Pro Ser Val Leu Lys 45	Ile Leu 15 Ser Gly 30 Phe Ile	Val Glu Cys

Thr Ile Phe Phe Lys Asp

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95

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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
                                                                      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
                                                                     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                            40
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
                                                                     240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
                                                                     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                                    90
cgc acc atc ttc ttc aag gac
                                                                     309
Arg Thr Ile Phe Phe Lys Asp
            100
<210> 247
<211> 103
<212> PRT
<213> Artificial
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      modif. frag.; CFP F1B, S65A, Y66W, and S72A mutations
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
               5
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                25
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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 75 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp 100 <210> 248 <211> 306 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F1B, S65A, Y66W, and S72A mutations, and posit. 1 Met removed <220> <221> CDS <222> (1)..(306) <400> 248 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 10 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 25 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys ace ace gge aag etg eee gtg eee tgg eee ace ete gtg ace ace tte 192 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240 Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

40

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306
 acc atc ttc ttc aag gac
 Thr Ile Phe Phe Lys Asp
           100
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        102
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        PRT
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        modif. frag.; CFP F1B, S65A, Y66W, and S72A mutations,
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        and posit. 1 Met removed
 <400> 249
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
             20
                                 25
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                             40
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
     50
                         55
 Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
                     70
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 Thr Ile Phe Phe Lys Asp
             100
 <210> 250
 <211> 309
 <212> DNA
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 <223> modif. frag.; CFP F1B,F64L ,S65T, and Y66W mutations
 <220>
 <221> CDS
 <222> (1)..(309)
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atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

<400> 250

1	5	10	15
		c ggc cac aag ttc n Gly His Lys Phe 25	
		c ggc aag ctg acc c Gly Lys Leu Thr	
		g ccc tgg ccc acc Pro Trp Pro Thr 60	
		c gcc cgc tac ccc e Ala Arg Tyr Pro 75	
		c atg ccc gaa ggc a Met Pro Glu Gly 90	
cgc acc atc ttc Arg Thr Ile Phe 100	5 5		309
<210> 251 <211> 103 <212> PRT <213> Artificia	al		
·			
<220> <223> modif. f:	cag.; CFP F1B,F6	54L ,S65T, and Y6	6W mutations
	cag.; CFP F1B,F6	54L ,S65T, and Y6	6W mutations
<223> modif. f: <400> 251 Met Val Ser Lys		of 4L ,S65T, and Y6 . Phe Thr Gly Val 10	
<223> modif. f: <400> 251 Met Val Ser Lys 1	Gly Glu Glu Leu 5	Phe Thr Gly Val	Val Pro Ile Leu 15
<223> modif. f: <400> 251 Met Val Ser Lys 1 Val Glu Leu Asp 20	Gly Glu Glu Leu 5 Gly Asp Val Asr	Phe Thr Gly Val 10 1 Gly His Lys Phe	Val Pro Ile Leu 15 Ser Val Ser Gly 30
<223> modif. f: <400> 251 Met Val Ser Lys 1 Val Glu Leu Asp 20 Glu Gly Glu Gly 35	Gly Glu Glu Leu 5 Gly Asp Val Asr Asp Ala Thr Tyr 40	Phe Thr Gly Val 10 1 Gly His Lys Phe 25	Val Pro Ile Leu 15 Ser Val Ser Gly 30 Leu Lys Phe Ile 45
<223> modif. f: <400> 251 Met Val Ser Lys 1 Val Glu Leu Asp 20 Glu Gly Glu Gly 35 Cys Thr Thr Gly 50	Gly Glu Glu Leu 5 Gly Asp Val Asr Asp Ala Thr Tyr 40 Lys Leu Pro Val 55	Phe Thr Gly Val 10 Gly His Lys Phe 25 Gly Lys Leu Thr	Val Pro Ile Leu 15 Ser Val Ser Gly 30 Leu Lys Phe Ile 45 Leu Val Thr Thr

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<210>
       252
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       306
<212>
      DNA
<213>
       Artificial
<220>
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       and posit. 1 Met removed
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       CDS
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      (1)..(306)
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gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
                                                                        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                                     10
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
                                                                        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc
                                                                       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc
                                                                       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50
                        55
acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg
                                                                       240
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65
                    70
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc
                                                                       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85
acc atc ttc ttc aag gac
                                                                       306
Thr Ile Phe Phe Lys Asp
            100
<210>
       253
<211>
       102
<212>
       PRT
<213>
       Artificial
<220>
       modif. frag.; CFP F1B, F64L , S65T, and Y66W mutations,
       and posit. 1 Met removed
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Arg Thr Ile Phe Phe Lys Asp

<400> 253

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 25 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 40 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 55 Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arq Thr Ile Phe Phe Lys Asp 100 <210> 254 <211> 309 <212> DNA <213> Artificial <220> <223> modif. frag.; BFP F1B, with Y66H mutation <220> <221> CDS <222> (1)..(309) <400> 254 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 ... 55 ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240 Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95

cgc acc atc ttc ttc aag gac
Arg Thr Ile Phe Phe Lys Asp

288

<210> 255

<211> 103

<212> PRT

<213> Artificial

100

<220>

<223> modif. frag.; BFP F1B, with Y66H mutation

<400> 255

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60

Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95

Arg Thr Ile Phe Phe Lys Asp 100

<210> 256

<211> 306

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1B, with Y66H mutation and posit. 1 Met removed

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	ggc gag gag Gly Glu Glu 5					48
	ggc gac gta Gly Asp Val 20					96
	gat gcc acc Asp Ala Thr					144
	aag ctg ccc Lys Leu Pro		Pro Thr			192
	ctg cag tgc Leu Gln Cys 70					. 240
	ttc aag tcc Phe Lys Ser 85					288
	ttc aag gac Phe Lys Asp 100					306
<210> 257 <211> 102 <212> PRT <213> Arti	ficial					
34 - 4	f. frag.; BF removed	P F1B, with	Y66H muta	tion and pos	sit. 1	
<400> 257						
Val Ser Lys 1	Gly Glu Glu 5	Leu Phe Thr	Gly Val	Val Pro Ile	Leu Val 15	
Glu Leu Asp	Gly Asp Val 20	Asn Gly His	Lys Phe	Ser Val Ser 30	Gly Glu	
Gly Glu Gly 35	Asp Ala Thr	Tyr Gly Lys	Leu Thr	Leu Lys Phe 45	Ile Cys	
Thr Thr Gly	Lys Leu Pro	Val Pro Trp 55		Leu Val Thr 60	Thr Phe	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 Thr Ile Phe Phe Lys Asp 100 <210> 258 <211> 309 <212> DNA <213> Artificial <220> <223> modif. frag.; BFP F1B, with F64L, Y66H mutations <220> <221> CDS <222> (1)..(309)<400> 258 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 25 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr ctg ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240 Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 90 cgc acc atc ttc ttc aag gac 309 Arg Thr Ile Phe Phe Lys Asp 100

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg

70

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<210> 259
 <211> 103
 <212> PRT
 <213>
       Artificial
 <220>
       modif. frag.; BFP F1B, with F64L, Y66H mutations
 <400> 259
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                 25
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                     70
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                 85
Arg Thr Ile Phe Phe Lys Asp
             100
 <210> 260
 <211> 306
 <212> DNA
 <213> Artificial
<220>
 <223>
       modif. frag.; BFP F1B, with F64L, Y66H mutations
       and posit. 1 Met removed
 <220>
 <221>
       CDS
 <222>
       (1)..(306)
 <400> 260
 gtg age aag ggc gag gag etg tte ace ggg gtg gtg eec ate etg gte
                                                                        48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                                     10
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
                                                                        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20
                                 25
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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	Ŀ
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 55 60	2
ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80)
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	3
acc atc ttc ttc aag gac 306 Thr Ile Phe Phe Lys Asp 100	5
<210> 261 <211> 102 <212> PRT <213> Artificial	
<220> <223> modif. frag.; BFP F1B, with F64L, Y66H mutations and posit. 1 Met removed	
<400> 261	
<pre><400> 261 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15</pre>	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 15 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 45 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 15 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 40 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 55 Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	

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<210> 262
<211>
      411
<212>
      DNA
      Artificial
<213>
<220>
<223>
      modif. frag.; YFP F2B (aa residues 104-240 of EYFP)
       and Met added @ posit. 1
<220>
<221> CDS
<222> (1)..(411)
<400> 262
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                                                                       48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
                                    10
acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac
                                                                       96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac
                                                                      144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc
                                                                      192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac
                                                                      240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
                                        75
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac
                                                                      288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                                    90
aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag
                                                                      336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
                                105
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc
                                                                      384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115
                            120
                                                125
act ctc ggc atg gac gag ctg tac aag
                                                                      411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130
                        135
<210> 263
<211>
      137
<212>
      PRT
<213> Artificial
<220>
<223>
      modif. frag.; YFP F2B (aa residues 104-240 of EYFP)
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and Met added @ posit. 1

<400> 263

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 1 5 10 15

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 20 25 30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn 35 40 45

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 50 55 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135

<210> 264

<211> 408

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; EGFP F2B(emerald), N146K, M153T, and I167T mutations $\left(\frac{1}{2}\right)$

<220>

<221> CDS

<222> (1)..(408)

<400> 264

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly

20	25	30
		50

					aag Lys											144
					aag Lys											192
					gag Glu 70											240
					atc Ile											288
					cag Gln											336
					ctg Leu											384
					ctg Leu											408
<210 <211 <212 <213	L> 1 2> I	265 136 PRT Arti	ficia	al												
<220 <223 muta			E. fi	rag.	; EGI	FP F2	2B (er	mera]	ld),	N146	5K, N	11537	Γ, ar	nd I:	167T	
<400)> 2	265														
Asp 1	Gly	Asn	Tyr	Lys 5	Thr	Arg	Ala	Glu	Val 10	Lys	Phe	Glu	Gly	Asp 15	Thr	
Leu	Val	Asn	Arg 20	Ile	Glu	Leu	Lys	Gly 25	Ile	Asp	Phe	Lys	Glu 30	Asp	Gly	
Asn	Ile	Leu 35	Gly	His	Lys	Leu	Glu 40	Tyr	Asn	Tyr	Asn	Ser 45	His	Lys	Val	
Tyr	Ile 50	Thr	Ala	Asp	Lys	Gln 55	Lys	Asn	Gly	Ile	Lys 60	Val	Asn	Phe	Lys	

Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 65 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 90 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 105 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 120 125 Leu Gly Met Asp Glu Leu Tyr Lys <210> 266 <211> 411 <212> DNA <213> Artificial <220> <223> modif. frag.; EGFP F2B(emerald), N146K, M153T, and I167T mutations and Met added @ posit. 1 <220> <221> CDS <222> (1)..(411) <400> 266 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 10 acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 25 ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aag 144 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192 Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 50 55 aag acc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240 Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag 336 Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu

110

105

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 1,15 120 act ctc ggc atg gac gag ctg tac aag 411 Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135 <210> 267 <211> 137 <212> PRT <213> Artificial <220> <223> modif. frag.; EGFP F2B(emerald), N146K, M153T, and I167T mutations and Met added @ posit. 1 <400> 267 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys

135

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<210> 268
<211> 408
<212> DNA
<213>
      Artificial
<220>
<223>
       modif. frag.; YFP F2B with Y203F mutation
<220>
       CDS
<221>
<222>
       (1)...(408)
<400> 268
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc
                                                                       48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
                                    10
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                       96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
                                                                      144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
        35
                            40
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag
                                                                      192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
    50
                        55
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac
                                                                      240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65
                    70
                                        75
                                                             80
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac
                                                                      288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
cac tac ctg age ttc cag tcc gcc ctg age aaa gac ccc aac gag aag
                                                                      336
His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act
                                                                      384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115
                            120
ctc ggc atg gac gag ctg tac aag
                                                                      408
Leu Gly Met Asp Glu Leu Tyr Lys
    130
<210> 269
<211> 136
<212> PRT
<213> Artificial
<220>
<223> modif. frag.; YFP F2B with Y203F mutation
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<400> 269
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
                        55
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                                    90
                85
His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100
                                105
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
                            120
Leu Gly Met Asp Glu Leu Tyr Lys
    130
<210> 270
<211>
      411
<212> DNA
<213> Artificial
<220>
<223>
      modif. frag.; YFP F2B with Y203F mutation + Met @ posit. 1
<220>
<221>
      CDS
<222> (1)..(411)
<400> 270
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac
                                                                       48
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10

96

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
20 25 30

5

35	ctg ggg Leu Gly												144
gtc tat atc Val Tyr Ile 50			ys Gln										192
aag atc cgc Lys Ile Arg 65													240
tac cag cag Tyr Gln Gln													288
aac cac tac Asn His Tyr													336
aag cgc gat Lys Arg Asp 115													384
act ctc ggc Thr Leu Gly 130		Glu L											411
			•										
<210> 271 <211> 137 <212> PRT <213> Arti	ficial						•						
<211> 137 <212> PRT <213> Arti <220>	ficial f. frag.	; YFP 1	F2B wi	th Y2	:03F	muta	ation	ı + N	Met @) pos	sit.	1	
<211> 137 <212> PRT <213> Arti <220>		; YFP 1	F2B wi	th Y2	:03F	muta	ation	ı + N	Met @) pos	sit. I	1	
<211> 137 <212> PRT <213> Arti <220> <223> modi	f. frag.											1	
<pre><211> 137 <212> PRT <213> Arti <220> <223> modi <400> 271 Met Asp Gly</pre>	f. frag. Asn Tyr 5	Lys Tl	nr Arg	Ala	Glu 10	Val	Lys	Phe	Glu	Gly 15	Asp		
<211> 137 <212> PRT <213> Arti <220> <223> modi <400> 271 Met Asp Gly 1	f. frag. Asn Tyr 5 Asn Arg 20	Lys Th	nr Arg lu Leu	Ala Lys 25	Glu 10 Gly	Val Ile	Lys Asp	Phe Phe	Glu Lys 30	Gly 15 Glu	Asp		
<pre><211> 137 <212> PRT <213> Arti <220> <223> modi <400> 271 Met Asp Gly 1 Thr Leu Val Gly Asn Ile</pre>	f. frag. Asn Tyr 5 Asn Arg 20 Leu Gly	Lys The Grant His Ly	nr Arg lu Leu ys Leu 40 ys Gln	Ala Lys 25 Glu	Glu 10 Gly Tyr	Val Ile Asn	Lys Asp Tyr	Phe Phe Asn 45	Glu Lys 30 Ser	Gly 15 Glu His	Asp Asp Asn	1	

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 90 Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 105 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 Thr Leu Gly Met Asp Glu Leu Tyr Lys <210> 272 <211> 408 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F2B with Y203H mutation <220> <221> CDS <222> (1)..(408) <400> 272 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly ... 20 25 aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 144 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 35 tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 192 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 50 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 65 80 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 cac tac ctg age cac cag tee gee etg age aaa gae eee aae gag aag 336 His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc ggg atc act 384

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

115 120 125

408

ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys

130 135

<210> 273

<211> 136

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F2B with Y203H mutation

<400> 273

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 55

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn - 85 90

His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 . 125

Leu Gly Met Asp Glu Leu Tyr Lys 130 135

<210> 274

<211> 411

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2B with Y203H mutation + Met @ posit. 1

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       CDS
<222>
       (1)...(411)
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                                                                       48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
                                    10
acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac
                                                                       96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
                                25
ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac
                                                                      144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
                            40
gtc tat atc atg gcc gac aag cag aag gac ggc atc aag gtg aac ttc
                                                                      192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
    50
aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac
                                                                      240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
                    70
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac
                                                                      288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
aac cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac gag
                                                                      336
Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100
                                105
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc
                                                                      384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115
                            120
act ctc ggc atg gac gag ctg tac aag
                                                                      411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
   130
<210> 275
<211> 137
<212> PRT
<213> Artificial
<220>
       modif. frag.; YFP F2B with Y203H mutation + Met @ posit. 1
<223>
<400>
      275
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
                5
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
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Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 55 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135 <210> 276 <211> 408 <212> DNA <213> Artificial <223> modif. frag.; CFP F2B with N146I mutation <220> <221> CDS <222> (1)..(408) <400> 276 gac ggc aac tac aag acc cgc qcc qaq qtq aaq ttc qaq qqc qac acc 48 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 5 ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 144 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 35 tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 192 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 50 55 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr

75 70 75 80

					atc Ile											288
					cag Gln											336
					ctg Leu											384
					ctg Leu											408
<210 <211 <212 <213	l> 1 2> I	277 136 PRT Artif	icia	al												
<220 <223		nodif	. fı	rag.;	: CFI	P F2E	3 wit	h Ni	.46I	muta	ation	1				
<400)> 2	277														
Asp 1	Gly	Asn	Tyr	Lys 5	Thr	Arg	Ala	Glu	Val 10	Lys	Phe	Glu	Gly	Asp 15	Thr	
Leu	Val	Asn	Arg 20	Ile	Glu	Leu	Lys	Gly 25	Ile	Asp	Phe	Lys	Glu 30	Asp	Gly	
Asn	Ile	Leu 35	Gly	His	Lys	Leu	Glu 40	Tyr	Asn	Tyr	Ile	Ser 45	His	Asn	Val	
Tyr	Ile 50	Met	Ala	Asp	Lys	Gln 55	Lys	Asn	Gly	Ile	Lys 60	Val	Asn	Phe	Lys	
Ile 65	Arg	His	Asn	Ile	Glu 70	Asp	Gly	Ser	Val	Gln 75	Leu	Ala	Asp	His	Tyr 80	
Gln	Gln	Asn	Thr	Pro 85	Ile	Gly	Asp	Gly	Pro 90	Val	Leu	Leu	Pro	Asp 95	Asn	•
His	Tyr	Leu	Ser 100	Thr	Gln	Ser	Ala	Leu 105	Ser	Lys	Asp	Pro	Asn 110	Glu	Lys	
Arg	Asp	His	Met	Val	Leu	Leu	Glu 120	Phe	Val	Thr	Ala	Ala 125	Gly	Ile	Thr	

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<210> 278
<211> 411
<212> DNA
<213> Artificial
<220>
      modif. frag.; CFP F2B w. N146I mutation and Met added @ posit. 1
<220>
<221>
       CDS
<222>
      (1)..(411)
<400> 278
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Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac
                                                                      96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac
                                                                     144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
        35
                            40
gtc tat atc atg gcc gac aag cag aag ggc atc aag gtg aac ttc
                                                                     192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
    50
                        55
aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac
                                                                     240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
                    70
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac
                                                                     288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85
aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag
                                                                     336
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100
                                105
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc
                                                                     384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115
                            120
act ctc ggc atg gac gag ctg tac aag
                                                                     411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
<210> 279
<211> 137
<212> PRT
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Leu Gly Met Asp Glu Leu Tyr Lys

130

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<220>
<223> modif. frag.; CFP F2B w. N146I mutation and Met added @ posit. 1
<400> 279
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
                                25
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
    50
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
                                        75
                    70
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85
                                    90
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100
                                105
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
       115
                            120
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130
<210> 280
<211> 408
<212> DNA
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<223> modif. frag.; CFP F2B with M153T mutation
<220>
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gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc
                                                                      48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
                5
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                      96
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Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly

20		25	30
aac atc ctg ggg cac Asn Ile Leu Gly His 35			er His Asn Val
tat atc act gcc gac Tyr Ile Thr Ala Asp 50			
atc cgc cac aac atc Ile Arg His Asn Ile 65			
cag cag aac acc ccc Gln Gln Asn Thr Pro 85			
cac tac ctg agc acc His Tyr Leu Ser Thr 100			
cgc gat cac atg gtc Arg Asp His Met Val 115			a Gly Ile Thr
ctc ggc atg gac gag Leu Gly Met Asp Glu 130			408
<210> 281 <211> 136 <212> PRT <213> Artificial			
<220> <223> modif. frag.	; CFP F2B wit	th M153T mutation	
<400> 281			
Asp Gly Asn Tyr Lys 1 5	Thr Arg Ala	Glu Val Lys Phe Gl 10	u Gly Asp Thr 15
Leu Val Asn Arg Ile 20	Glu Leu Lys	Gly Ile Asp Phe Ly 25	rs Glu Asp Gly 30
Asn Ile Leu Gly His	Lys Leu Glu 40	Tyr Asn Tyr Asn Se	
Tyr Ile Thr Ala Asp	Lys Gln Lys 55	Asn Gly Ile Lys Va	l Asn Phe Lys

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 65 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 120 Leu Gly Met Asp Glu Leu Tyr Lys 130 135 <210> 282 <211> 411 <212> DNA <213> Artificial <223> modif. frag.; CFP F2B w. M153T mutation and Met added @ posit. 1 <220> <221> CDS <222> (1)..(411) <400> 282 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn 35 gto tat atc act gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192 Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 50 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag 336 Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile

115 120 125

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act ctc ggc atg gac gag ctg tac aag
                                                                     411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130
                        135
<210> 283
<211> 137
<212> PRT
<213> Artificial
<220>
<223> modif. frag.; CFP F2B w. M153T mutation and Met added @ posit. 1
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Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
                       55
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
           100
                                105
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130
                        135
<210> 284
<211> 408
<212> DNA
<213> Artificial
<220>
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<223> modif. frag.; CFP F2B with N146I, M153T mutations

<220> <221> CDS <222> (1).	. (408)				
	_		gtg aag ttc gag Val Lys Phe Glu 10		48
			atc gac ttc aag Ile Asp Phe Lys		96
			aac tac atc agc Asn Tyr Ile Ser 45		144
			ggc atc aag gtg Gly Ile Lys Val 60		192
			gtg cag ctc gcc Val Gln Leu Ala 75		240
			ccc gtg ctg ctg Pro Val Leu Leu 90		288
			agc aaa gac ccc Ser Lys Asp Pro		336
	Met Val Leu		gtg acc gcc gcc Val Thr Ala Ala 125	Gly Ile Thr	384
	gac gag ctg Asp Glu Leu	_			408
<210> 285 <211> 136 <212> PRT <213> Arti	ficial				
<220> <223> modi	f. frag.; CF	P F2B with N1	l46I, M153T muta	tions	
<400> 285			·		
Asp Gly Asn	Tyr Lys Thr 5	Arg Ala Glu	Val Lys Phe Glu 10	Gly Asp Thr 15	
Leu Val Asn	Arg Ile Glu 20	Leu Lys Gly 25	Ile Asp Phe Lys	Glu Asp Gly 30	

35 40 45	
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 50 55 60	
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 65 70 75 80	
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 95	
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 110	
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 125	
Leu Gly Met Asp Glu Leu Tyr Lys 130 135	•
<210> 286 <211> 411	
<212> DNA <213> Artificial	
<213> Artificial <220> <223> modif. frag.; CFP F2B with N146I, M153T mutations	
<213> Artificial <220> <223> modif. frag.; CFP F2B with N146I, M153T mutations and Met added @ posit. 1 <220> <221> CDS	48
<pre><213> Artificial <220> <223> modif. frag.; CFP F2B with N146I, M153T mutations</pre>	48
<pre><213> Artificial <220> <223> modif. frag.; CFP F2B with N146I, M153T mutations</pre>	
<pre><213> Artificial <220> <223> modif. frag.; CFP F2B with N146I, M153T mutations</pre>	96

65 70 75 80

tac cag cag a Tyr Gln Gln A					ro Asp
aac cac tac c Asn His Tyr L			Leu Ser Ly		
aag cgc gat c Lys Arg Asp H 115					
act ctc ggc a Thr Leu Gly Mo 130					411
<210> 287 <211> 137 <212> PRT <213> Artific	cial				
	frag.; CF t added @]	P F2B with N posit. 1	146I, M153T	mutations	
<400> 287					
Met Asp Gly A	sn Tyr Lys 5	Thr Arg Ala	Glu Val Lys	s Phe Glu G	
Thr Leu Val A		Glu Leu Lys 25	Gly Ile As	p Phe Lys G 30	lu Asp
Gly Asn Ile Lo	eu Gly His	Lys Leu Glu 40	Tyr Asn Ty:	r Ile Ser H 45	is Asn
Val Tyr Ile Ti 50	hr Ala Asp	Lys Gln Lys 55	Asn Gly Ile	e Lys Val A	sn Phe
Lys Ile Arg H	is Asn Ile 70	Glu Asp Gly	Ser Val Gli 75	n Leu Ala A	sp His 80
Tyr Gln Gln A	sn Thr Pro 85	Ile Gly Asp	Gly Pro Vai	l Leu Leu Pr 99	
Asn His Tyr Le	eu Ser Thr 00	Gln Ser Ala 105		s Asp Pro As	sn Glu
Lys Arg Asp H: 115	is Met Val	Leu Leu Glu 120	Phe Val Th	r Ala Ala G 125	ly Ile

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Thr Leu Gly Met Asp Glu Leu Tyr Lys
130 135
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<210> 288 <211> 408 <212> DNA <213> Artificial	
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<220> <221> CDS <222> (1)(408)	
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ctg gtg aac cgc atc gag ctg aag ggc at Leu Val Asn Arg Ile Glu Leu Lys Gly Il 20 25	
aac atc ctg ggg cac aag ctg gag tac aa Asn Ile Leu Gly His Lys Leu Glu Tyr As 35 40	
tat atc atg gcc gac aag cag aag aac gg Tyr Ile Met Ala Asp Lys Gln Lys Asn Gl 50 55	
atc cgc cac aac atc gag gac ggc agc gt Ile Arg His Asn Ile Glu Asp Gly Ser Va 65 70	
cag cag aac acc ccc atc ggc gac ggc cc Gln Gln Asn Thr Pro Ile Gly Asp Gly Pr 85 90	o Val Leu Leu Pro Asp Asn
cac tac ctg agc acc cag tcc gcc ctg ag His Tyr Leu Ser Thr Gln Ser Ala Leu Se 100	gc aaa gac ccc aac gag aag 336 er Lys Asp Pro Asn Glu Lys 110
cgc gat cac atg gtc ctg ctg gag ttc gt Arg Asp His Met Val Leu Leu Glu Phe Va 115 120	
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 130	408
<210> 289 <211> 136 <212> PRT <213> Artificial	

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<223> modif. frag.; CFP F2B with V163A mutation
<400> 289
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
                            40
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
                                        75
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
              85
                                   90
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100
                                105
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
       115
                            120
Leu Gly Met Asp Glu Leu Tyr Lys
    130
<210> 290
<211> 411
<212> DNA
<213> Artificial
<220>
<223> modif. frag.; CFP F2B w. V163A mutation and Met added @ posit. 1
<220>
<221> CDS
<222> (1)..(411)
<400> 290
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac
                                                                      48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
               5
1
acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac
                                                                      96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
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<220>

20 25 30

	144
gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 50 55 60	192
aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 70 75 80	240
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95	288
aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110	336
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125	384
act ctc ggc atg gac gag ctg tac aag Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135	411
<210> 291 <211> 137 <212> PRT <213> Artificial	
<220> <223> modif. frag.; CFP F2B w. V163A mutation and Met added @ pos	it. 1
	it. 1
<223> modif. frag.; CFP F2B w. V163A mutation and Met added @ pos	it. 1
<223> modif. frag.; CFP F2B w. V163A mutation and Met added @ pos <400> 291 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp	it. 1
<pre><223> modif. frag.; CFP F2B w. V163A mutation and Met added @ pos <400> 291 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 1</pre>	it. 1
<pre><223> modif. frag.; CFP F2B w. V163A mutation and Met added @ pos <400> 291 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 1</pre>	it. 1

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 90 Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135 <210> 292 <211> 408 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F2B with N146I, V163A mutations <220> <221> CDS <222> (1)..(408) <400> 292 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 144 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 35 tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 192 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50 atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac 288 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag aag 336 His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 ege gat cae atg gte etg etg gag tte gtg ace gee gee ggg ate act 384

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

115 120 125

ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys

130

408

<210> 293

<211> 136

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F2B with N146I, V163A mutations

<400> 293

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 1 5 10 15

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 20 25 30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 35 40 45

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50 55 60

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 75 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 95

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

Leu Gly Met Asp Glu Leu Tyr Lys 130 135

<210> 294

<211> 411

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F2B with N146I, V163A mutations

and Met added @ posit. 1

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<220>
<221> CDS
<222> (1)..(411)
<400> 294
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Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
                                                                      96
acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac
                                                                     144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc
                                                                     192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
    50
                        55
aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac
                                                                     240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac
                                                                     288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
aac cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag
                                                                     336
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
                                105
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc
                                                                     384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
                            120
                                                125
act ctc ggc atg gac gag ctg tac aag
                                                                     411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
<210> 295
<211> 137
<212> PRT
<213> Artificial
<220>
<223> modif. frag.; CFP F2B with N146I, V163A mutations
      and Met added @ posit. 1
<400> 295
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
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Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp

	Gly	Asn	Ile 35	Leu	Gly	His	Lys	Leu 40	Glu	Tyr	Asn	Tyr	Ile 45	Ser	His	Asn	
	Val	Tyr 50	Ile	Met	Ala	Asp	Lys 55	Gln	Lys	Asn	Gly	Ile 60	Lys	Ala	Asn	Phe	
	Lys 65	Ile	Arg	His	Asn	Ile 70	Glu	Asp	Gly	Ser	Val 75	Gln	Leu	Ala	Asp	His 80	
	Tyr	Gln	Gln	Asn	Thr 85	Pro	Ile	Gly	Asp	Gly 90	Pro	Val	Leu	Leu	Pro 95	Asp	
	Asn	His	Tyr	Leu 100	Ser	Thr	Gln	Ser	Ala 105	Leu	Ser	Lys	Asp	Pro 110	Asn	Glu	
	Lys	Arg	Asp 115	His	Met	Val	Leu	Leu 120	Glu	Phe	Val	Thr	Ala 125	Ala	Gly	Ile	
	Thr	Leu 130	Gly	Met	Asp	Glu	Leu 135	Tyr	Lys								
•	<210 <211 <212 <213	.> 4 ?> [296 108 DNA Artii	ficia	al												
	<220 <223		nodi	E. fi	rag.;	: CFI	P F2E	3 wit	h Mi	153T,	. V1	L63A	mut	atio	ons		
	<220 <221 <222	.> (CDS	. (408	3)												
	<400 gac Asp 1	ggc	96 aac Asn	tac Tyr	aag Lys 5	acc Thr	cgc Arg	gcc Ala	gag Glu	gtg Val 10	aag Lys	ttc Phe	gag Glu	ggc Gly	gac Asp 15	acc Thr	48
						gag Glu											96
						aag Lys											144
						aag Lys											192

65	c atc gag n Ile Gli 70									240
cag cag aac ac Gln Gln Asn Th										288
cac tac ctg ag His Tyr Leu Se 10	r Thr Glr									336
cgc gat cac at Arg Asp His Me 115		Leu C								384
ctc ggc atg ga Leu Gly Met As 130										408
<210> 297 <211> 136 <212> PRT <213> Artific	ial									
<220> <223> modif.	frag.; CE	P F2B	with Mi	L53T, V	163A	mut	atio	ons		
<400> 297			i							
Asp Gly Asn Ty	r Lys Thr 5	Arg A	Ala Glu	Val Lys 10	Phe	Glu	Gly	Asp 15	Thr ·	
	5 .			10			_	15		
1 Leu Val Asn Ar	5 . g Ile Glu	Leu I	Lys Gly 25	10	Phe	Lys	Glu 30	15 Asp	Gly	
Leu Val Asn Ar 20 Asn Ile Leu Gl	5 g Ile Glu y His Lys	Leu I Leu G	Lys Gly 25 Glu Tyr 40	<pre>10 Ile Asp Asn Tyr</pre>	Phe Asn	Lys Ser 45	Glu 30	Asp Asn	Gly Val	
Leu Val Asn Ar 20 Asn Ile Leu Gl 35 Tyr Ile Thr Al	5 .g Ile Glu y His Lys	Leu I Leu G 4 GIn I 55	Lys Gly 25 Glu Tyr 40 Lys Asn	<pre>10 Ile Asp Asn Tyr Gly Ile</pre>	Phe Asn Lys 60	Lys Ser 45 Ala	Glu 30 His	Asp Asn Phe	Gly Val Lys	
Leu Val Asn Ar 20 Asn Ile Leu Gl 35 Tyr Ile Thr Al 50 Ile Arg His As	5 g Ile Glu y His Lys a Asp Lys n Ile Glu 70	Leu I Leu G G G G G S G S G S S S S S S S S S S S	Lys Gly 25 Glu Tyr 40 Lys Asn	10 Ile Asp Asn Tyr Gly Ile Val Gln 75	Phe Asn Lys 60 Leu	Lys Ser 45 Ala	Glu 30 His Asn	Asp Asn Phe	Gly Val Lys Tyr 80	
Leu Val Asn Ar 20 Asn Ile Leu Gl 35 Tyr Ile Thr Al 50 Ile Arg His As 65	5 g Ile Glu y His Lys a Asp Lys n Ile Glu 70 r Pro Ile 85	Leu I Leu I Gln I SS	Lys Gly 25 Glu Tyr 40 Lys Asn Gly Ser	10 Ile Asp Asn Tyr Gly Ile Val Gln 75 Pro Val 90	Phe Asn Lys 60 Leu Leu	Lys Ser 45 Ala Ala	Glu 30 His Asn Asp	Asp Asp Asp 95	Gly Val Lys Tyr 80 Asn	

Leu Gly Met Asp Glu Leu Tyr Lys 130 135	
<210> 298 <211> 411 <212> DNA <213> Artificial	
<220> <223> modif. frag.; CFP F2B with M153T, V163A mutations and Met added @ posit. 1	
<220> <221> CDS <222> (1)(411)	
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acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 20 25 30	96
ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn 35 40 45	144
gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 50 55 60	192
aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 70 75 80	240
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95	288
aac cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110	336
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125	384
act ctc ggc atg gac gag ctg tac aag Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135	411
<210> 299 <211> 137	

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F2B with M153T, V163A mutations
 and Met added @ posit. 1

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Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 50 55 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95

Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110

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atc cgc ca Ile Arg H: 65														240
cag cag aa Gln Gln Aa														288
cac tac co														336
cgc gat ca Arg Asp H: 1:														384
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Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala A 65 70 75	asp His Tyr 80
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu P	Pro Asp Asn 95
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro A	sn Glu Lys 10
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aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110	336												
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Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc
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Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
                            40
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag
                                                                      192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
                        55
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atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac
                                                                      240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac
                                                                      288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag
                                                                      336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
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ege gat cac atg gte etg etg gag tte gtg ace gee geg ate act
                                                                      384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
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ctc ggc atg gac gag ctg tac aag
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Gly	Asn	Ile 35	Leu	Gly	His	Lys	Leu 40	Glu	Tyr	Asn	Tyr	Ile 45	Ser	His	Asn	
	tat Tyr 50															192
	atc Ile															240

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Gly	Asn	Ile 35	Leu	Gly	His	Lys	Leu 40	Glu	Tyr	Asn	Tyr	Ile 45	Ser	His	Asn		
Val	Tyr 50	Ile	Met	Ala	Asp	Lys 55	Gln	Lys	Asn	Gly	Ile 60	Lys	Val	Asn	Phe		
Lys 65	Ile	Arg	His	Asn	Ile 70	Glu	Asp	Gly	Ser	Val 75	Gln	Leu	Ala	Asp	His 80		
Tyr	Gln	Gln	Asn	Thr 85	Pro	Ile	Gly	Asp	Gly 90	Pro	Val	Leu	Leu	Pro 95	Asp		
Asn	His	Tyr	Leu 100	Ser	Tyr	Gln	Ser	Ala 105	Leu	Ser	Lys	Asp	Pro 110	Asn	Glu		
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aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 35 40 45	44
tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys 50 55 60	92
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cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 95	88
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 110	36
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 . 120 125	84
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atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac

Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp

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aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cacLys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His65707580	240
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95	288
aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110	336
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125	384
act ctc ggc atg gac gag ctg tac aag Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135	411
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Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn 35 40 45	
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 50 55 60	
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 70 75 80	

Tyr	Gln	Gln	Asn	Thr 85	Pro	Ile	Gly	Asp	Gly 90	Pro	Val	Leu	Leu	Pro 95	Asp	
Asn	His	Tyr	Leu 100	Ser	Tyr	Gln	Ser	Ala 105	Leu	Ser	Lys	Asp	Pro 110	Asn	Glu	
Lys	Arg	Asp 115	His	Met	Val	Leu	Leu 120	Glu	Phe	Val	Thr	Ala 125	Ala	Gly	Ile	
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ctg Leu	gtg Val	aac Asn	cgc Arg 20	atc Ile	gag Glu	ctg Leu	aag Lys	ggc Gly 25	atc Ile	gac Asp	ttc Phe	aag Lys	gag Glu 30	gac Asp	ggc Gly	96
aac Asn	atc Ile	ctg Leu 35	ggg Gly	cac His	aag Lys	ctg Leu	gag Glu 40	tac Tyr	aac Asn	tac Tyr	atc Ile	agc Ser 45	cac His	aac Asn	gtc Val	144
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atc Ile 65	cgc Arg	cac His	aac Asn	atc Ile	gag Glu 70	gac Asp	ggc Gly	agc Ser	gtg Val	cag Gln 75	ctc Leu	gcc Ala	gac Asp	cac His	tac Tyr 80	240
cag Gln	cag	aac Asn	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac Asn	288
	GIII	71011	1111	85	110	Cly		0-7	90	vai	LCu	LCu	110	95	1.01.	

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 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
 ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac
                                                                       144
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
 gtc tat atc acc gcc gac aag cag aag ggc atc aag gtg aac ttc
                                                                       192
 Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
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                         55
 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac
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 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
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 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc cac gac
                                                                       288
 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
 aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag
                                                                       336
 Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
                                 105
 aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc
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 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
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Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 50 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110

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115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys

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Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
20 25 30

48

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val

35

40

45

tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50 55 60	192										
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 65 70 75 80	240										
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 95	288										
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 110	336										
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100 105 110

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Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

120

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      and Met added @ posit. 1
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Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
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Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
   50 55
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
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Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
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Thr Leu Gly Met Asp Glu Leu Tyr Lys
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		ctg Leu 35										_			-	144
		atg Met														192
		cac His														240
		aac Asn														288
		ctg Leu														336
		cac His 115													act Thr	384
		atg Met	_		_		_									408
<210 <211 <212 <213	l> 1 2> I	321 136 PRT Artif	icia	al												
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<400)> 3	321														
Asp 1	Gly	Asn	Tyr	Lys 5	Thr	Arg	Ala	Glu	Val 10	Lys	Phe	Glu	Gly	Asp 15	Thr	
Leu	Val	Asn	Arg 20	Ile	Glu	Leu	Lys	Gly 25	Ile	Asp	Phe	Lys	Glu 30	Asp	Gly	
Asn	Ile	Leu 35	Gly	His	Lys	Leu	Glu 40	Tyr	Asn	Tyr	Ile	Ser 45	His	Asn	Val	

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 55 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 120 Leu Gly Met Asp Glu Leu Tyr Lys 130 135 <210> 322 <211> 411 <212> DNA <213> Artificial <220> <223> modif. frag.; CGFP F2B, N146I, V163A, and T203Y mutations and Met added @ posit. 1 <220> <221> CDS <222> (1)..(411)<400> 322 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp acc ctq qtq aac cqc atc qaq ctq aaq qqc atc qac ttc aaq qaq qac 96 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac 144 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn 35 gtc tat atc atg gcc gac aag cag aac ggc atc aag gcc aac ttc 192 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 50 55 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65

		cag Gln														288
		tac Tyr														336
		gat Asp 115														384
		ggc Gly														411
<210 <211 <211 <211	1 > 1 2 > 1	323 137 PRT Artií	ficia	al								•				
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Met 1	Asp	Gly	Asn	Tyr 5	Lys	Thr	Arg	Ala	Glu 10	Val	Lys	Phe	Glu	Gly 15	Asp	
Thr	Leu	Val	Asn 20	Arg	Ile	Glu	Leu	Lys 25	Gly	Ile	Asp	Phe	Lys 30	Glu	Asp	
Gly	Asn	Ile 35	Leu	Gly	His	Lys	Leu 40	Glu	Tyr	Asn	Tyr	Ile 45	Ser	His	Asn	
Val	Tyr 50	Ile	Met	Ala	Asp	Lys 55	Gln	Lys	Asn	Gly	Ile 60	Lys	Ala	Asn	Phe	
Lys 65	Ile	Arg	His	Asn	Ile 70	Glu	Asp	Gly	Ser	Val 75	Gln	Leu	Ala	Asp	His 80	
Tyr	Gln	Gln	Asn	Thr 85	Pro	Ile	Gly	Asp	Gly 90	Pro	Val	Leu	Leu	Pro 95	Asp	
Asn	His	Tyr	Leu 100	Ser	Tyr	Gln	Ser	Ala 105	Leu	Ser	Lys	Asp	Pro 110	Asn	Glu	
Lys	Arg	Asp 115	His	Met	Val	Leu	Leu 120	Glu	Phe	Val	Thr	Ala 125	Ala	Gly	Ile	

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                                                                       96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                                25
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
                                                                      144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
                                                                      192
tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
                        55
atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac
                                                                      240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
                    70
                                        75
cag cag aac acc ccc atc ggc qac ggc ccc qtq ctq ctg ccc qac aac
                                                                      288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag
                                                                      336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                                105 -
                                                                      384
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act
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Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

120

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ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn 35 40 45	144										
gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 50 55 60	192										
aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cacLys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His65707580	240										
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95	288										
aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110	336										
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125	384										
act ctc ggc atg gac gag ctg tac aag Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135	411										
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Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 20 25 30											
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn 35 40 45											
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 50 55 60											

65 70 75 .	p His 80											
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pr 85 90 95												
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro As 100 105 110	n Glu											
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gl 115 120 125	y Ile											
Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135	•											
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<222> (1)(400)												
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<400> 328 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc ga Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly As	p Thr c ggc 96											
<pre><400> 328 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc ga Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly As 1</pre>	p Thr c ggc 96 p Gly c gtc 144											
<pre><400> 328 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc ga Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly As 1</pre>	p Thr c ggc 96 p Gly c gtc 144 n Val											
<pre><400> 328 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc ga Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly As 1</pre>	p Thr c ggc 96 p Gly c gtc 144 n Val c aag 192 e Lys c tac 240											

cac tac ctg age tac cag tee gee ctg age aaa gae eee aac gag aag 336 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 ctc ggc atg gac gag ctg tac aag 408 Leu Gly Met Asp Glu Leu Tyr Lys 130 <210> 329 <211> 136 <212> PRT<213> Artificial <220> <223> modif. frag.; CGFP F2B, N146I, M153T, V163A, and T203Y mutations <400> 329 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly 20 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val 35 40 Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50 Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr 65 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 95 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 Leu Gly Met Asp Glu Leu Tyr Lys 130 135

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       and Met added @ posit. 1
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                                                                       48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
acc ctg gtg aac cgc atc gag ctg aaq ggc atc gac ttc aaq gaq gac
                                                                       96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac
                                                                      144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
        35
gtc tat atc acc gcc gac aag cag aag ggc atc aag gcc aac ttc
                                                                      192
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
    50
                        55
aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac
                                                                      240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
                    70
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac
                                                                      288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85
aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag
                                                                      336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggq atc
                                                                      384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115
                            120
act ctc ggc atg gac gag ctg tac aag
                                                                      411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130
<210> 331
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and Met added @ posit. 1

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Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
                        55
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                                   90
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
                               105
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
Thr Leu Gly Met Asp Glu Leu Tyr Lys
                       135
    130
<210> 332
<211> 408
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atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac ta Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Ty 65 70 75 80	
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aa Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asp 85 90 95	
cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aa His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Ly 100 105 110	
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc ac Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Th	
ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 130 135	408
<210> 333 <211> 136	
<212> PRT <213> Artificial	
<213> Artificial <220>	
<220> <223> modif. frag.; BFP F2B with Y145F mutation	r
<220> <223> modif. frag.; BFP F2B with Y145F mutation <400> 333 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Th	
<220> <223> modif. frag.; BFP F2B with Y145F mutation <400> 333 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Th 1 5 10 15 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gl	Y
<pre><213> Artificial <220> <223> modif. frag.; BFP F2B with Y145F mutation <400> 333 Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Th 1</pre>	Y 1

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 120 Leu Gly Met Asp Glu Leu Tyr Lys 130 <210> 334 <211> 411 <212> DNA <213> Artificial <223> modif. frag.; BFP F2B w. Y145F mutation and Met added @ posit. 1 <220> <221> CDS <222> (1)..(411) <400> 334 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp ggc aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac 144 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn 35 gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 50 55 aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag 336 Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile

115 120 125

act ctc ggc atg gac gag ctg tac aag Thr Leu Gly Met Asp Glu Leu Tyr Lys

130 135

411

<210> 335

<211> 137

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F2B w. Y145F mutation and Met added @ posit. 1

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Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
20 25 30

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn 35 40 45

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 50 55 60

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His 65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 85 90 95

Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 110

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 125

Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 135

<210> 336

<211> 408

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2B with S175G mutation

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                                    10
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc
                                                                       96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc
                                                                      144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag
                                                                      192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
atc cgc cac aac atc gag gac ggc gtg cag ctc gcc gac cac tac
                                                                      240
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac
                                                                      288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85
cac tac ctg age tac cag tee gee etg age aaa gae eee aae gag aag
                                                                      336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100
                                105
ege gat cae atg gte etg etg gag tte gtg ace gee geg gte act
                                                                      384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115
                            120
                                                                      408
ctc ggc atg gac gag ctg tac aag
Leu Gly Met Asp Glu Leu Tyr Lys
    130
<210> 337
<211>
      136
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       modif. frag.; Venus F2B with S175G mutation
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                5
                                                        15
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
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25

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 105 Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 125 Leu Gly Met Asp Glu Leu Tyr Lys 130 135 <210> 338 <211> 411 <212> DNA <213> Artificial <220> <223> modif. frag.; Venus F2B with S175G mutation and Met added @ posit. 1 <220> <221> CDS <222> (1)..(411) <400> 338 atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 25 ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn 40 gtc tat atc atg gcc gac aag cag aac ggc atc aag gtg aac ttc 192 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe 50

240

aag atc cgc cac aac atc gag gac ggc gtg cag ctc gcc gac cac

Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His 65 70 75 80

			ggc ccc gtg co Gly Pro Val Le 90									
Asn His Tyr			ctg agc aaa ga Leu Ser Lys As									
			ttc gtg acc go Phe Val Thr A									
act ctc ggc Thr Leu Gly				41								
<210> 339 <211> 137 <212> PRT <213> Artificial												
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<400> 339												
Met Asp Gly .	Asn Tyr Lys 5	Thr Arg Ala	Glu Val Lys Pl 10	ne Glu Gly Asp 15								
	Asn Arg Ile 20	Glu Leu Lys 25	Gly Ile Asp Ph	ne Lys Glu Asp 30								
Gly Asn Ile 35	Leu Gly His	Lys Leu Glu 40	Tyr Asn Tyr As									
Val Tyr Ile i	Met Ala Asp	Lys Gln Lys 55	Asn Gly Ile Ly	ys Val Asn Phe								
Lys Ile Arg	His Asn Ile 70	Glu Asp Gly	Gly Val Gln Le 75	eu Ala Asp His 80								
Tyr Gln Gln	Asn Thr Pro 85	Ile Gly Asp	Gly Pro Val Le 90	eu Leu Pro Asp 95								
_	Leu Ser Tyr 100	Gln Ser Ala 105	Leu Ser Lys As	sp Pro Asn Glu 110								
Lys Arg Asp 1	His Met Val	Leu Leu Glu 120	Phe Val Thr A	la Ala Gly Ile 25								

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Thr Leu Gly Met Asp Glu Leu Tyr Lys
130 135
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<210> 340 <211> 408 <212> DNA <213> Artifi	.cial											
<220> <223> modif. frag.; Venus F2B w. M153T, S175G mutations												
<220> <221> CDS <222> (1)	(408)											
<400> 340 gac ggc aac t Asp Gly Asn T						48						
ctg gtg aac c Leu Val Asn A						96						
aac atc ctg o Asn Ile Leu 0 35						144						
tat atc acc of Tyr Ile Thr A	la Asp Lys					192						
atc cgc cac a Ile Arg His A 65						240						
cag cag aac a Gln Gln Asn T						288						
cac tac ctg a His Tyr Leu S			Ser Lys			336						
cgc gat cac a Arg Asp His M 115	itg gtc ctg	ctg gag tto Leu Glu Pho 120	gtg acc Val Thr	gcc gcc ggg Ala Ala Gly 125	atc act Ile Thr	384						
ctc ggc atg c Leu Gly Met A 130	sp Glu Leu					408						
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Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                                25
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
                            40
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr
                    70
                                        75
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
               85
                                    90
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100
                                105
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
       115
                            120
Leu Gly Met Asp Glu Leu Tyr Lys
    130
<210> 342
<211> 411
<212> DNA
<213> Artificial
<220>
     modif. frag.; Venus F2B w. M153T, S175G mutations
      and Met added @ posit. 1
<220>
<221> CDS
<222> (1)..(411)
<400> 342
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac
                                                                      48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac
                                                                      96
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	Thr	Leu	Val	Asn 20	Arg	Ile	Glu	Leu	Lys 25	Gly	Ile	Asp	Phe	Lys 30	Glu	Asp		
						cac His												144
						gac Asp												192
						atc Ile 70												240
						ccc Pro												288
						tac Tyr												336
						gtc Val												384
						gag Glu												411
<210> 343 <211> 137 <212> PRT <213> Artificial																		
<220> <223> modif. frag.; Venus F2B w. M153T, S175G mutations and Met added @ posit. 1																		
<400> 343																		
	Met 1	Asp	Gly	Asn	Tyr 5	Lys	Thr	Arg	Ala	Glu 10	Val	Lys	Phe	Glu	Gly 15	Asp		
	Thr	Leu	Val	Asn 20.	Arg	Ile	Glu	Leu	Lys 25	Gly	Ile	Asp	Phe	Lys 30	Glu	Asp		
	Gly	Asn	Ile 35	Leu	Gly	His	Lys	Leu 40	Glu	Tyr	Asn	Tyr	Asn 45	Ser	His	Asn		
	Val	Tyr 50	Ile	Thr	Ala	Asp	Lys 55	Gln	Lys	Asn	Gly	Ile 60	Lys	Val	Asn	Phe		•
	_									_	_	_		_				

Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His

65 70 75 80

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 90 Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 105 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 120 Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 <210> 344 <211> 408 <212> DNA <213> Artificial <220> <223> modif. frag.; Venus F2B w. V163A, S175G mutations <220> <221> CDS <222> (1)..(408) <400> 344 gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96 Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 144 Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 35 tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 192 Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50 atc cgc cac aac atc gag gac ggc gtg cag ctc gcc gac cac tac 240 Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr 70 cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac aac 288 Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 95 cac tac ctg age tac cag tee gee ctg age aaa gae eee aac gag aag 336 His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys 100 105 cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr

115 120 125

ctc ggc atg gac gag ctg tac aag Leu Gly Met Asp Glu Leu Tyr Lys 130

r Lys

408

<210> 345

<211> 136

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F2B w. V163A, S175G mutations

<400> 345

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr 1 5 10 15

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
20 25 30

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val 35 40 45

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys 50 55 60

Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr 65 70 75 80

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn 85 90 95

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
100 105 110

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 125

Leu Gly Met Asp Glu Leu Tyr Lys 130 135

<210> 346

<211> 411

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2B w. V163A, S175G mutations

and Met added @ posit. 1

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<220>
<221> CDS
<222> (1)..(411)
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac
                                                                      48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac
                                                                      96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac
                                                                     144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
gtc tat atc atg qcc gac aag cag aag aac ggc atc aag qcc aac ttc
                                                                     192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
aag atc cgc cac aac atc gag gac ggc gtg cag ctc gcc gac cac
                                                                     240
Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc gac
                                                                     288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85
                                    90
aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag
                                                                     336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc
                                                                     384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
act ctc ggc atg gac gag ctg tac aag
                                                                     411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130
<210> 347
<211> 137
<212> PRT
<213> Artificial
      modif. frag.; Venus F2B w. V163A, S175G mutations
       and Met added @ posit. 1
<400> 347
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
                5
                                    10
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Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp

Gly	Asn	Ile 35	Leu	Gly	His	Lys	Leu 40	Glu	Tyr	Asn	Tyr	Asn 45	Ser	His	Asn	
Val	Tyr 50	Ile	Met	Ala	Asp	Lys 55	Gln	Lys	Asn	Gly	Ile 60	Lys	Ala	Asn	Phe	
Lys 65	Ile	Arg	His	Asn	Ile 70	Glu	Asp	Gly	Gly	Val 75	Gln	Leu	Ala	Asp	His 80	
Tyr	Gln	Gln	Asn	Thr 85	Pro	Ile	Gly	Asp	Gly 90	Pro	Val	Leu	Leu	Pro 95	Asp	
Asn	His	Tyr	Leu 100	Ser	Tyr	Gln	Ser	Ala 105	Leu	Ser	Lys	Asp	Pro 110	Asn	Glu	
Lys	Arg	Asp 115	His	Met	Val	Leu	Leu 120	Glu	Phe	Val	Thr	Ala 125	Ala	Gly	Ile	
Thr	Leu 130	Gly	Met	Asp	Glu	Leu 135	Tyr	Lys								
<210 <211 <212 <213	L> 4 2> I	348 108 ONA Artif	ficia	al												
<220 <223		nodif	E. fi	rag.;	: Ver	nus E	F2B,	M153	3T, V	/163/	A, S1	.75G	muta	ation	ns	
<220 <221 <222	L> (CDS (1)	. (408	3)												
	ggc				acc Thr											48
ctg Leu	gtg Val	aac Asn	cgc Arg 20	atc Ile	gag Glu	ctg Leu	aag Lys	ggc Gly 25	atc Ile	gac Asp	ttc Phe	aag Lys	gag Glu 30	gac Asp	ggc Gly	96
					aag Lys											144
					aag Lys											192

atc cgc cac Ile Arg His 65												240
cag cag aac Gln Gln Asn												288
cac tac ctg His Tyr Leu												336
cgc gat cac Arg Asp His 115												384
ctc ggc atg Leu Gly Met 130		_	r Lys									408
<210> 349 <211> 136 <212> PRT <213> Artif	ficial											
<220> <223> modif	f. frag.	; Venus	F2B,	M153	3T, V	/163/	A, SI	L75G	muta	ation	າຣ	
<400> 349												
<400> 349 Asp Gly Asn 1	Tyr Lys 5	Thr Ar	g Ala	Glu	Val 10	Lys	Phe	Glu	Gly	Asp 15	Thr	
Asp Gly Asn	5				10					15		
Asp Gly Asn	Arg Ile	Glu Le	u Lys	Gly 25	10	Asp	Phe	Lys	Glu 30	15 Asp	Gly	
Asp Gly Asn Leu Val Asn Asn Ile Leu	Arg Ile 20 Gly His	Glu Le	u Lys u Glu 40 n Lys	Gly 25	10 Ile Asn	Asp Tyr	Phe Asn	Lys Ser 45	Glu 30	15 Asp Asn	Gly Val	
Asp Gly Asn Leu Val Asn Asn Ile Leu 35 Tyr Ile Thr	Arg Ile 20 Gly His Ala Asp	Glu Le	u Lys u Glu 40 n Lys	Gly 25 Tyr Asn	10 Ile Asn Gly	Asp Tyr Ile	Phe Asn Lys 60	Lys Ser 45	Glu 30 His	Asp Asn Phe	Gly Val Lys	
Asp Gly Asn Leu Val Asn Asn Ile Leu 35 Tyr Ile Thr 50 Ile Arg His	Arg Ile 20 Gly His Ala Asp Asn Ile	Glu Les Lys Les Lys Gl 55 Glu As 70	u Lys u Glu 40 n Lys p Gly	Gly 25 Tyr Asn	10 Ile Asn Gly Val	Asp Tyr Ile Gln 75	Phe Asn Lys 60 Leu	Lys Ser 45 Ala	Glu 30 His Asn	Asp Asn Phe	Cly Val Lys Tyr 80	

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr 115 120 125

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130
<210>
       350
<211>
       411
<212>
      DNA
<213>
       Artificial
<220>
<223>
      modif. frag.; Venus F2B, M153T, V163A, S175G mutations
       and Met added @ posit. 1
<220>
<221>
      CDS
<222>
      (1)...(411)
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atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac
                                                                       48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac
                                                                       96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac
                                                                      144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
        35
gtc tat atc acc gcc gac aag cag aac ggc atc aag gcc aac ttc
                                                                      192
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
aag atc cgc cac aac atc gag gac ggc gtg cag ctc gcc gac cac
                                                                      240
Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His
65
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac
                                                                      288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85
aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gaq
                                                                      336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100
aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc
                                                                      384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115
                            120
                                                                      411
act ctc ggc atg gac gag ctg tac aag
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130
                        135
<210> 351
<211>
      137
<212> PRT
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Leu Gly Met Asp Glu Leu Tyr Lys

<213> Artificial <220> <223> modif. frag.; Venus F2B, M153T, V163A, S175G mutations and Met added @ posit. 1 <400> 351 Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp 5 10 · 15 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp 25 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe 55 Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp 90 Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu 100 105 Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile 115 120 Thr Leu Gly Met Asp Glu Leu Tyr Lys 130 <210> 352

<210> 352
<211> 348
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; YFP F1C (aa residues 1-117 of EYFP) with posit.1 Met removed

<220>
<221> CDS
<222> (1)..(348)

gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg gtc Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val

1	5	10	15	
	gac gta aac ggc Asp Val Asn Gly			
	gcc acc tac ggc Ala Thr Tyr Gly 40			
	ctg ccc gtg ccc Leu Pro Val Pro 55	Trp Pro Thr		
	cag tgc ttc gcc Gln Cys Phe Ala 70			
	aag tcc gcc atg Lys Ser Ala Met 85			
	aag gac gac ggc Lys Asp Asp Gly			
aag ttc gag ggc Lys Phe Glu Gly 115				348
<210> 353 <211> 116 <212> PRT <213> Artificia	al			
	rag.; YFP F1C (a Met removed	a residues 1-	117 of EYFP) wi	th
<400> 353			•	
Val Ser Lys Gly	Glu Glu Leu Phe 5	Thr Gly Val V	Val Pro Ile Leu 15	Val
Glu Leu Asp Gly 20	Asp Val Asn Gly	His Lys Phe 9	Ser Val Ser Gly 30	Glu
Gly Glu Gly Asp 35	Ala Thr Tyr Gly 40	Lys Leu Thr	Leu Lys Phe Ile 45	Cys
Thr Thr Gly Lys	Leu Pro Val Pro 55		Leu Val Thr Thr 60	Phe
Gly Tyr Gly Leu 65	Gln Cys Phe Ala 70	Arg Tyr Pro 7	Asp His Met Lys	Arg 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

Lys Phe Glu Gly 115

<210> 354 <211> 351

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1C, with F46L mutation

<220>

<221> CDS

<222> (1)..(351)

<400> 354

atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

1 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr

50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc 351

Val Lys Phe Glu Gly 115

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<212> PRT
<213> Artificial
<223> modif. frag.; YFP F1C, with F46L mutation
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
                                   10
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
                            40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100
Val Lys Phe Glu Gly
       115
<210> 356
<211> 348
<212> DNA
<213> Artificial
<223> modif. frag.; YFP F1C w. F46L mutation & posit. 1 Met removed
<220>
<221> CDS
<222> (1)..(348)
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
                                                                      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
               5
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
                                                                      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
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<211> 117

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			20					25					30			
					acc Thr											144
					ccc Pro											192
					tgc Cys 70											240
					tcc Ser											288
					gac Asp											336
		gag Glu 115											•			348
<210 <211 <212 <213	l> 1 2> I 3> 1	357 116 PRT Artif	Eicia	al												
<220 <223		nodif	. fr	ag.;	YFI	P F10	C w.	F46I	, mut	atio	on &	posi	it. 1	L Met	removed	
<400)> 3	357														
Val 1	Ser	Lys	Gly	Glu 5	Glu	Leu	Phe	Thr	Gly 10	Val	Val	Pro	Ile	Leu 15	Val	
Glu	Leu	Asp	Gly 20	Asp	Val	Asn	Gly	His 25	Lys	Phe	Ser	Val	Ser 30	Gly	Glu	
Gly	Glu	Gly 35	Asp	Ala	Thr	Tyr	Gly 40	Lys	Leu	Thr	Leu	Lys 45	Leu	Ile	Cys	
Thr	Thr 50	Gly	Lys	Leu	Pro	Val 55	Pro	Trp	Pro	Thr	Leu 60	Val	Thr	Thr	Phe	
Gly 65	Tyr	Gly	Leu	Gln	Cys 70	Phe	Ala	Arg	Tyr	Pro 75	Asp	His	Met	Lys	Arg 80	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95

Lys Phe Glu Gly 115 <210> 358 <211> 351 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F1C with K79R mutation <220> <221> CDS <222> (1)..(351) <400> 358 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 tte gge tae gge etg eag tge tte gee ege tae eee gae eac atg ege 240 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg 65 288 egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 95 ege ace ate the the aag gae gae gge aac tae aag ace ege gee gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 351 gtg aag ttc gag ggc Val Lys Phe Glu Gly 115

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
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ggc gag ggc g Gly Glu Gly A 35										144
acc acc ggc a Thr Thr Gly I 50						u Val				192
ggc tac ggc c Gly Tyr Gly I 65										240
cac gac ttc t His Asp Phe H										288
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aag ttc gag g Lys Phe Glu C 115										348
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Glu Leu Asp C	5 Gly Asp 20 Asp Ala	Val Asn Thr Tyr	Gly H: 25 Gly Ly 40	is Lys 5 ys Leu	Phe Se Thr Le	r Val u Lys 45 u Val	Ser 30 Phe	15 Gly Ile	Glu Cys	

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His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                           40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
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Val Lys Phe Glu Gly
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gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag
                                                                     96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
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		ggc Gly 35														144
		ggc Gly														192
		ggc Gly														240
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		ttc Phe														336
		gag Glu 115														348
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Gly	Glu	Gly 35	Asp	Ala	Thr	Tyr	Gly 40	Lys	Leu	Thr	Leu	Lys 45	Phe	Ile	Cys	
Thr	Thr 50	Gly	Lys	Leu	Pro	Val 55	Pro	Trp	Pŗo	Thr	Leu 60	Val	Thr	Thr	Phe	

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                            40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50
                        55
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                                        75
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
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Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
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Val Lys Phe Glu Gly
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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Giu Leu Ast	ggc gac Gly Asp 20											96
ggc gag ggc Gly Glu Gly 35												144
acc acc ggo Thr Thr Gly 50												192
ggc tac ggc Gly Tyr Gly 65												240
cac gac tto His Asp Phe												288
acc atc ttc Thr Ile Phe												336
aag ttc gag Lys Phe Glu 115	Gly											348
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His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
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                        55
Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
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Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
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Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
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Val Lys Phe Glu Gly
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Glu Leu Asp	ggc gac Gly Asp 20											96
ggc gag ggc Gly Glu Gly 35												144
acc acc ggc Thr Thr Gly 50		Pro V										192
ggc tac ggc Gly Tyr Gly 65												240
cac gac ttc His Asp Phe												288
acc atc ttc Thr Ile Phe												336
aag ttc gag Lys Phe Glu 115												348
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Val Ser Lys	Gly Glu 5 Gly Asp 20	et rem Glu L Val A	eu Phe	Thr His	Gly 10 Lys	Val Phe	Val Ser	Pro Val	Ile Ser 30	Leu 15 Gly	Glu	
Val Ser Lys 1 Glu Leu Asp Gly Glu Gly	Gly Glu 5 Gly Asp 20 Asp Ala	Glu L Val A	eu Phe sn Gly Yr Gly 40	Thr His 25 Lys	Gly 10 Lys Leu	Val Phe Thr	Val Ser Leu	Pro Val Lys 45	Ile Ser 30	Leu 15 Gly Ile	Glu Cys	

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His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arq

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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
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Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
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Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
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Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
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Val Lys Phe Glu Gly
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 55 60	192
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
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His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

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85

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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
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Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
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Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
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Val Lys Phe Glu Gly
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 55 60	192
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 . Sel Cly Glu 30 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	

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His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arq

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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
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Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
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Val Lys Phe Glu Gly
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gag Glu																96
ggc Gly																144
acc Thr																192
ggc Gly 65																240
cac His																288
acc Thr																336
aag Lys																348
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Glu	Leu	Asp	Gly 20	Asp	Val	Asn	Gly	His 25	Lys	Phe	Ser	Val	Ser 30	Gly	Glu	
Gly	Glu	Gly 35	Asp	Ala	Thr	Tyr	Gly 40	Lys	Leu	Thr	Leu	Lys 45	Phe	Ile	Cys	
Thr	Thr 50	Gly	Lys	Leu	Pro	Val 55	Pro	Trp	Pro	Thr	Leu 60	Val	Thr	Thr	Phe	

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly 115 <210> 386 <211> 351 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F1C with S65A mutation <220> <221> CDS <222> (1)..(351) <400> 386 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 10 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 tte gee tae gge etg eag tge tte gee ege tae eee gae eac atg aag 240 Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 egg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 cgc acc atc ttc ttc aag gac ggc aac tac aag acc cgc gcc gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 105 gtg aag ttc gag ggc 351 Val Lys Phe Glu Gly 115

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                            40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50
Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
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Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
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Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
Val Lys Phe Glu Gly
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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Giu Leu	Asp G	gc gac ly Asp 0												96
ggc gag Gly Glu														144
acc acc Thr Thr 50														192
gcc tac Ala Tyr 65														240
cac gac His Asp														288
acc atc Thr Ile	Phe P													336
aag ttc Lys Phe														348
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Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly 115 <210> 390 <211> 351 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F1C , S65A, Y66W, and S72A mutations <220> <221> CDS <222> (1)..(351) <400> 390 atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr tte gee tgg gge etg eag tge tte gee ege tae eee gae eac atg aag 240 Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu ege ace ate the the aag gae gae gge aac tae aag ace ege gee gaq 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 105 gtg aag ttc gag ggc 351 Val Lys Phe Glu Gly

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85 .
                                      90
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
             100
                                  105
Val Lys Phe Glu Gly
        115
<210> 392
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       & posit. 1 Met removed
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1	5	10	15
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	gcc acc tac ggc aag Ala Thr Tyr Gly Lys 40		
	ctg ccc gtg ccc tgg Leu Pro Val Pro Trp 55		
	cag tgc ttc gcc cgc Gln Cys Phe Ala Arg 70		
	aag tcc gcc atg ccc Lys Ser Ala Met Pro 85		
	aag gac gac ggc aac Lys Asp Asp Gly Asn 105		
aag ttc gag ggc Lys Phe Glu Gly 115			348
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	rag.; CFP F1C , S65A, 1 Met removed	Y66W, and S72A muta	ations
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1	5	Gly Val Val Pro Ile 10	Leu Val 15
1		10	15
Glu Leu Asp Gly 20	5 Asp Val Asn Gly His	Lys Phe Ser Val Ser	15 Gly Glu
Glu Leu Asp Gly 20 Gly Glu Gly Asp 35	Asp Val Asn Gly His 25 Ala Thr Tyr Gly Lys	Lys Phe Ser Val Ser 30 Leu Thr Leu Lys Phe 45	Gly Glu Ile Cys

85 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly 115 <210> 394 <211> 351 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F1C , F64L, S65T, and Y66W mutations <220> <221> CDS <222> (1)..(351) <400> 394 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240 Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 80 egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 ege ace ate the the aag gae gae gge aac tae aag ace ege gee gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 105 110 gtg aag ttc gag ggc 351 Val Lys Phe Glu Gly

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arq

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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
                            40
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65
                    70
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100
Val Lys Phe Glu Gly
       115
<210> 396
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       & posit. 1 Met removed
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gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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	ggc gac Gly Asp 20											96
ggc gag ggc Gly Glu Gly 35												144
acc acc ggc Thr Thr Gly 50			al Pro									192
acc tgg ggc Thr Trp Gly 65												240
cac gac ttc His Asp Phe												288
acc atc ttc Thr Ile Phe												336
aag ttc gag Lys Phe Glu 115												348
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<213> Arti	LICIAI											
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Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly <210> 398 <211> 351 <212> DNA <213> Artificial <220> <223> modif. frag.; BFP F1C with Y66H mutation <220> <221> CDS <222> (1)..(351) <400> 398 atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 10 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc 240 Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg 65 egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 cgc acc atc ttc ttc aag gac ggc aac tac aag acc cgc gcc gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 105 351 gtg aag ttc gag ggc Val Lys Phe Glu Gly

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

85

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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50
Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
                   70
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
               85
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
           100
Val Lys Phe Glu Gly
       115
<210> 400
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg 65 70 75 80	240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
aag ttc gag ggc Lys Phe Glu Gly 115	348
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly 115 <210> 402 <211> 351 <212> DNA <213> Artificial <220> <223> modif. frag.; BFP F1C w. F64L, Y66H mutations <220> <221> CDS <222> (1)..(351) <400> 402 atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc 240 Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg 65 egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Glu Glu - 85 90 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 351 gtg aag ttc gag ggc Val Lys Phe Glu Gly

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arq

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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100
                                105
Val Lys Phe Glu Gly
       115
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      & posit. 1 Met removed
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
                                   10
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•	ggc gac Gly Asp 20											96
ggc gag ggc Gly Glu Gly 35				y Lys								144
acc acc ggc Thr Thr Gly 50		Pro '										192
ggc cac ggc Gly His Gly 65												240
cac gac ttc His Asp Phe												288
acc atc ttc Thr Ile Phe												336
aag ttc gag Lys Phe Glu 115												348
<210> 405 <211> 116 <212> PRT			٠									
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<220> <223> modi & po: <400> 405 Val Ser Lys 1	f. frag. sit. 1 M Gly Glu 5 Gly Asp 20	Glu :	moved Leu Ph Asn Gl	e Thr Y His 25 Y Lys	Gly 10 Lys	Val Phe	Val Ser	Pro Val	Ile Ser 30	15 Gly	Glu	
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Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly 115 <210> 406 <211> 369 <212> DNA <213> Artificial <220> modif. frag.; YFP F2C and Met added @ position 1 <223> <220> <221> CDS <222> (1)..(369) <223> YFP F2C corresponds to aa residues 118-239 of YFP <400> 406 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser 20 cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg 144 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val 35 aac ttc aag atc cgc cac aac atc qag qac qgc aqc qtq caq ctc qcc 192 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 50 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu 65 ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc 288 Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro 85 95 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 ggg atc act ctc ggc atg gac gag ctg tac aag 369 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arq

85

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 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
         35
                             40
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
     50
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85
                                                         95
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
             100
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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<221>
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       (1)..(366)
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gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag
                                                                       48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
```

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20 25 30	96
aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35 40 45	144
ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 70 75 80	240
gac aac cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366
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Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1 10 15	
1 5 10 15 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20 Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn	

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 105 Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 <210> 410 <211> 369 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F2C w. Y203F mutation and Met added @ posit. 1 <220> <221> CDS <222> (1)..(369) <400> 410 atg gac acc ctg gtg aac cgc atc gag ctg aag gqc atc gac ttc aaq 48 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg 144 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val 35 40 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 50 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu ccc gac aac cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc 288 Pro Asp Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 105 369 ggg atc act ctc ggc atg gac gag ctg tac aag Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115

Asp Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn

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<210> 411
<211> 123
<212> PRT
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<220>
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Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
                        55
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
                    70
Pro Asp Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro
                85
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
<210> 412
<211> 366
<212> DNA
<213> Artificial
<223> modif. frag.; YFP F2C with Y203H mutation
<220>
<221> CDS
<222> (1)..(366)
<400> 412
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag
                                                                      48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
```

gac ggc aac Asp Gly Asn				u Glu							96
aac gtc tat Asn Val Tyr 35											144
ttc aag atc Phe Lys Ile 50											192
cac tac cag His Tyr Gln 65											240
gac aac cac Asp Asn His											288
gag aag cgc Glu Lys Arg				u Glu							336
atc act ctc Ile Thr Leu 115	Gly Met										366
<210> 413 <211> 122 <212> PRT <213> Arti	ficial	,									
<220> <223> modi	f. frag.	; YFP F2	C with	Y203H	muta	ation	1			·	
<400> 413											
Asp Thr Leu 1	Val Asn 5	Arg Ile	Glu Le	u Lys 10	Gly	Ile	Asp	Phe	Lys 15	Glu	
· Asp Gly Asn	Ile Leu 20	Gly His	Lys Le 25		Tyr	Asn	Tyr	Asn 30	Ser	His	
Asn Val Tyr 35	Ile Met	Ala Asp	Lys Gl 40	n Lys	Asn	Gly	Ile 45	Ĺys	Val	Asn	
Phe Lys Ile 50	Arg His	Asn Ile 55	Glu As	p Gly	Ser	Val 60	Gln	Leu	Ala	Asp	
His Tyr Gln											

85 90 Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 105 Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120 <210> 414 <211> 369 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F2C w. Y203H mutation and Met added @ posit. 1 <220> <221> CDS <222> (1)..(369) <400> 414 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg 144 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val 35 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 50 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu 65 ccc gac aac cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc 288 Pro Asp Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro 85 336 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 105 ggg atc act ctc ggc atg gac gag ctg tac aag 369 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys

Asp Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn

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       123
 <212>
       PRT
 <213>
       Artificial
 <220>
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Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
                            40
        35
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50
                        55
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65
Pro Asp Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro
                85
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
                                105
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115
<210> 416
<211> 366
<212> DNA
<213> Artificial
<220>
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<220>
<221>
       CDS
<222>
       (1)..(366)
       CFP F2C corresponds to residues 118-239 of YFP
<400> 416
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                                                                       48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
```

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His 20 25 30	96
aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35 40 45	144
ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 65 70 75 80	240
gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366
<210> 417 <211> 122 <212> PRT <213> Artificial	
<220> <223> modif. frag.; CFP F2C with N146I mutation	
<223> modif. frag.; CFP F2C with N146I mutation	
<223> modif. frag.; CFP F2C with N146I mutation <400> 417 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
<223> modif. frag.; CFP F2C with N146I mutation <400> 417 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1 5 10 15 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His	
<pre><223> modif. frag.; CFP F2C with N146I mutation <400> 417 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1</pre>	

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys <210> 418 <211> 369 <212> DNA Artificial <213> <220> modif. frag.; CFP F2C w. N146I mutation and Met added @ posit. 1 <223> <220> <221> CDS <222> (1)..(369) <400> 418 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc 96 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser 25 cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg 144 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 55 240 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro 85 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 105 ggg atc act ctc ggc atg gac gag ctg tac aag 369 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn

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<210> 419
<211> 123
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<213> Artificial
<220>
<223>
      modif. frag.; CFP F2C w. N146I mutation and Met added @ posit. 1
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Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
                                25
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
                        55
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
                    70
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
                85
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115
<210> 420
<211>
       366
<212>
      DNA
<213> Artificial
<220>
<223> modif. frag.; CFP F2C with M153T mutation
<220>
<221> CDS
<222> (1)..(366)
<400> 420
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag
                                                                      48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
```

20 25 30	96
aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35 40 45	144
ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 75 80	240
gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc ggc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366
<210> 421 <211> 122 <212> PRT <213> Artificial	
<220> <223> modif. frag.; CFP F2C with M153T mutation	
<220>	
<220> <223> modif. frag.; CFP F2C with M153T mutation	
<220> <223> modif. frag.; CFP F2C with M153T mutation <400> 421 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
<pre><220> <223> modif. frag.; CFP F2C with M153T mutation <400> 421 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1 5 10 15 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His</pre>	
<pre><220> <223> modif. frag.; CFP F2C with M153T mutation <400> 421 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1 5 10 15 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20 25 30 Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn</pre>	

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys <210> 422 <211> 369 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F2C w. M153T mutation + Met @ posit. 1 <220> <221> CDS <222> (1)..(369) <400> 422 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser 20 cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg 144 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 50 55 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu - 65 70 75 ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro . 85 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 ggg atc act ctc ggc atg gac gag ctg tac aag 369 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn

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<210> 423
<211> 123
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<213> Artificial
<220>
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Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
                    70
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
                85
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115
                            120
<210> 424
<211> 366
<212> DNA
<213> Artificial
<223> modif. frag.; CFP F2C w. N146I, M153T mutations
<220>
<221> CDS
<222> (1)..(366)
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag
                                                                      48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
```

ASP GIY ASH	atc ctg Ile Leu 20											96
aac gtc tat Asn Val Tyr 35												144
ttc aag atc Phe Lys Ile 50												192
cac tac cag His Tyr Gln 65												240
gac aac cac Asp Asn His												288
gag aag cgc Glu Lys Arg												336
atc act ctc Ile Thr Leu 115												366
<210> 425 <211> 122			•									
<212> PRT <213> Arti	ficial											
<213> Arti <220>	ficial f. frag.	; CFP F	2C w.	N146	51,	M153	ЗТ г	nutat	ions	8		
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<213> Arti <220> <223> modi	f. frag.										Glu	
<213> Arti <220> <223> modi <400> 425 Asp Thr Leu	f. frag. Val Asn 5	Arg Il	e Glu	Leu	Lys 10	Gly	Ile	Asp	Phe	Lys 15		
<213> Arti <220> <223> modi <400> 425 Asp Thr Leu 1	f. frag. Val Asn 5 Ile Leu 20	Arg Il	e Glu	Leu Leu 25	Lys 10 Glu	Gly Tyr	Ile Asn	Asp Tyr	Phe Ile 30	Lys 15 Ser	His	
<213> Arti <220> <223> modi <400> 425 Asp Thr Leu 1 Asp Gly Asn Asn Val Tyr	f. frag. Val Asn 5 Ile Leu 20	Arg Il	e Glu s Lys D Lys 40	Leu Leu 25	Lys 10 Glu Lys	Gly Tyr Asn	Ile Asn Gly	Asp Tyr Ile 45	Phe Ile 30	Lys 15 Ser Val	His Asn	

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 105 Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 <210> 426 <211> 369 <212> DNA <213> Artificial <220> modif. frag.; CFP F2C w. N146I, M153T mutations <223> and Met added @ posit. 1 <220> <221> CDS <222> (1)..(369) atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc 96 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser 25 cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg 144 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val aac tte aag ate ege cac aac ate gag gac ege age gtg cag ete gee 192 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro 85 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 105 ggg atc act ctc ggc atg gac gag ctg tac aag 369 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys

120

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<210> 427
<211> 123
<212> PRT
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       and Met added @ posit. 1
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                5
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
          100
                                105
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
       115
                            120
<210> 428
<211> 366
<212> DNA
<213> Artificial
<220>
<223> modif. frag.; CFP F2C with V163A mutation
<220>
<221> CDS
<222>
     (1)..(366)
<400> 428
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Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1
                                    10
                                                        15
```

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20 25 30	96
aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn 35 40 45	144
ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 65 70 75 80	240
gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc ggc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366
<210> 429 <211> 122 <212> PRT <213> Artificial	
<220> <223> modif. frag.; CFP F2C with V163A mutation	
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Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1 5 10 15	
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20 25 30	
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn	

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 <210> 430 <211> 369 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F2C w. V163A mutation and Met added @ posit. 1 <220> <221> CDS <222> (1)..(369) <400> 430 atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48 Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys 96 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc 144 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro 85 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 105 110 ggg atc act ctc ggc atg gac gag ctg tac aag 369 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120 <210> 431

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn

90

85

<211> 123

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 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
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 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
                             40
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
                 85
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
         115
 <210> 432
 <211> 366
 <212> DNA
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 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
                                     10
 gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac
                                                                       96
 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His
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aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aa Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Ly 35 40 45	
ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag cg Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Le 50 55 60	
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ct His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Le 65 70 75	
gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa ga Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys As 85 90	
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gc Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr A 100 105 1:	
atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366
<210> 433 <211> 122 <212> PRT <213> Artificial	
(213) Altilitial	
<220> <223> modif. frag.; CFP F2C w. N146I, V163A mutation <400> 433	ons
<220> <223> modif. frag.; CFP F2C w. N146I, V163A mutation	·
<220> <223> modif. frag.; CFP F2C w. N146I, V163A mutation <400> 433 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Pl	he Lys Glu 15 le Ser His
<pre><220> <223> modif. frag.; CFP F2C w. N146I, V163A mutatio <400> 433 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Pl 1</pre>	he Lys Glu 15 le Ser His 0
<pre><220> <223> modif. frag.; CFP F2C w. N146I, V163A mutatio <400> 433 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Pl 1</pre>	he Lys Glu 15 le Ser His 0 ys Ala Asn
<pre><220> <223> modif. frag.; CFP F2C w. N146I, V163A mutation <400> 433 Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Pl 1</pre>	he Lys Glu 15 le Ser His 0 ys Ala Asn eu Ala Asp

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110

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gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc
                                                                       96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc
                                                                      144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
                                                                      192
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
                        55
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc
                                                                      288
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
                                105
                                                                      369
ggg atc act ctc ggc atg gac gag ctg tac aag
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115
                            120
<210> 435
<211>
      123
<212>
      PRT
<213> Artificial
<220>
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Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys

Met added @ posit. 1

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Glu A	sp Gl	y Asn 20	Ile	Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Tyr 30	Ile	Ser	
His A	sn Va 35	l Tyr	Ile	Met	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Ala	
	he Ly	s Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Ser 60	Val	Gln	Leu	Ala	
Asp H 65	is Ty	r Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro A	.sp As	n His	Tyr 85	Leu	Ser	Thr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn G	lu Ly	s Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly I	le Th		Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
<210><211><212><213>	366 DNA	ifici	al												
<220> <223>		if. f	rag.	; CF	P F20	C w.	M153	3T, V	/163 <i>l</i>	A mı	ıtat:	ions			
<220> <221> <222>	CDS	(36	6)												
	436 cc ct hr Le														48
	gc aa ly As														96

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn

	ag atc ys Ile 0														192
	ac cag yr Gln														240
	ac cac sn His														288
	ag cgc ys Arg														336
	ct ctc hr Leu 115										·				366
<210><211><211><212><213>	122 PRT	ficia	al												
<220> <223>		f. fi	rag.;	; CFI	P F20	C w.	M153	3T, V	71637	A mi	ıtati	lons			
<400>	437														
	437 hr Leu	Val	Asn 5	Arg	Ile	Glu	Leu	Lys 10	Gly	Ile	Asp	Phe	Lys 15	Glu	
Asp Th			5					10					15		
Asp Ti	hr Leu	Ile 20	5 Leu	Gly	His	Lys	Leu 25	10 Glu	Tyr	Asn	Tyr	Asn 30	15 Ser	His	
Asp G	hr Leu ly Asn al Tyr 35 ys Ile	Ile 20	5 Leu Thr	Gly Ala	His Asp	Lys Lys 40	Leu 25 Gln	10 Glu Lys	Tyr Asn	Asn Gly	Tyr Ile 45	Asn 30 Lys	15 Ser Ala	His Asn	
Asp Gi	hr Leu ly Asn al Tyr 35 ys Ile	Ile 20 Ile Arg	5 Leu Thr	Gly Ala Asn	His Asp Ile 55	Lys Lys 40	Leu 25 Gln Asp	10 Glu Lys Gly	Tyr Asn Ser	Asn Gly Val 60	Tyr Ile 45 Gln	Asn 30 Lys Leu	15 Ser Ala Ala	His Asn Asp	
Asp Gi Asp Gi Asn Va Phe Ly 50 His Ty 65	hr Leu ly Asn al Tyr 35 ys Ile	Ile 20 Ile Arg	5 Leu Thr His	Gly Ala Asn Thr	His Asp Ile 55	Lys Lys 40 Glu	Leu 25 Gln Asp	10 Glu Lys Gly Asp	Tyr Asn Ser Gly 75	Asn Gly Val 60	Tyr Ile 45 Gln Val	Asn 30 Lys Leu Leu	Ser Ala Ala	His Asn Asp Pro 80	

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Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
<210> 438
<211> 369
<212> DNA
<213> Artificial
<220>
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<221> CDS
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gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc
                                                                      96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc
                                                                      144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
                            40
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc
                                                                      192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
                        55
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
                    70
                                        75
                                                                      288
ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
                                105 -
ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                      369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
                            120
<210> 439
<211> 123
<212> PRT
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<223> modif. frag.; CFP F2C w. M153T, V163A mutations
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and Met added @ posit. 1

V#01	-															
Met 1	Asp	Thr	Leu	Val 5	Asn	Arg	Ile	Glu	Leu 10	Lys	Gly	Ile	Asp	Phe 15	Lys	
Glu	Asp	Gly	Asn 20	Ile	Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Tyr 30	Asn	Ser	
His	Asn	Val 35	Tyr	Ile	Thr	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Ala	
Asn	Phe 50	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Ser 60	Val	Gln	Leu	Ala	
Asp 65	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro	Asp	Asn	His	Tyr 85	Leu	Ser	Thr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn	Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly	Ile	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
<210 <211 <212 <213	L> 3 2> I	140 366 DNA Artii	ficia	al												
<220 <223		nodii	E. fi	cag.	; CFI	? F20	C, N:	1461,	, M15	53T,	and	V16:	3A mi	ıtat:	ions	
<220 <221 <222	L> (CDS (1)	. (366	5)												
	acc				cgc Arg											48
					Gly 333											96
					gcc Ala											144

Phe Lys Ile A	gc cac aac rg His Asn							192
cac tac cag ca His Tyr Gln G 65								240
gac aac cac to Asp Asn His Ty								288
gag aag cgc ga Glu Lys Arg As 10						a Āla		336
atc act ctc go Ile Thr Leu G 115								366
<210> 441 <211> 122 <212> PRT <213> Artific	cial		·				·	
<220> <223> modif.	frag.; CF	P F2C, N	146I, M1	53T, and	V163A	mutati	ons.	
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Asp Thr Leu Va	5 · le Leu Gly		10			15 e Ser		
Asp Thr Leu Va	5 Le Leu Gly	His Lys	10 Leu Glu 25	Tyr Asn	Tyr Il	15 e Ser	His	
Asp Thr Leu Vall Asp Gly Asn II Asn Val Tyr II	5 le Leu Gly) le Thr Ala	His Lys Asp Lys 40	Leu Glu 25 Gln Lys	Tyr Asn Asn Gly	Tyr II 30 Ile Ly 45	e Ser	His His	
Asp Thr Leu Vallage Asp Gly Asn In 20 Asn Val Tyr In 35 Phe Lys Ile An	5 le Leu Gly le Thr Ala	His Lys Asp Lys 40 Ile Glu 55	Leu Glu 25 Gln Lys Asp Gly	Tyr Asn Asn Gly Ser Val	Tyr II 30 Ile Ly 45 Gln Le	e Ser s Ala	His Asn Asp	
Asp Thr Leu Vall Asp Gly Asn II 20 Asn Val Tyr II 35 Phe Lys Ile An 50 His Tyr Gln G	5 le Leu Gly le Thr Ala rg His Asn ln Asn Thr 70	His Lys Asp Lys 40 Ile Glu 55	Leu Glu 25 Gln Lys Asp Gly Gly Asp	Tyr Asn Asn Gly Ser Val 60 Gly Pro 75	Tyr II 30 Ile Ly 45 Gln Le	e Ser s Ala u Ala	His Asn Asp Pro 80	

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115
 <210>
       442
 <211>
        369
 <212>
       DNA
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 <223>
        and Met added @ posit. 1
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 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
                                 25
 cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc
                                                                       144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
         35
                             40
 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc
                                                                       192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
                         55
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                       240
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc
                                                                       288
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
                 85
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
             100
                                 105
ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                      369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 <210> 443
 <211> 123
 <212> PRT
 <213> Artificial
 <220>
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<223> modif. frag.; CFP F2C, N146I, M153T, and V163A mutations

	and Me	t adde	d @ p	osit	. 1									
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Glu Asr	Gly As		Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Tyr 30	Ile	Ser	
His Asr	ı Val T	yr Ile	Thr	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Ala	
Asn Phe	e Lys I	le Arg	His	Asn 55	Ile	Glu	Asp	Gly	Ser 60	Val	Gln	Leu	Ala	
Asp His	Tyr G	ln Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro Asp	Asn H	is Tyr 85	Leu	Ser	Thr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn Glı		rg Asp 00	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly Ile	e Thr Le	eu Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
<210><211><212><213>	444 366 DNA Artific	cial												
<220> <223>	modif.	frag.	; CGF	P F2	2C w.	. M15	53T,	T203	3Y mı	ıtat:	ions			
	CDS (1)(; CGFP F;		respo	onds	to 1	resid	lues	118	-239	of S	/FP			
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gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac

Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35 40 45	
ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctc ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 75 80	240
gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366
<210> 445 <211> 122 <212> PRT <213> Artificial	
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Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20 Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20 Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35 Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 30 Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35 Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	

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<210> 446
<211>
       369
<212>
       DNA
       Artificial
<213>
<220>
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<223>
       Met added @ posit. 1
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<221>
      CDS
<222>
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gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc
                                                                       96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg
                                                                      144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc
                                                                      192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
                        55
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc
                                                                      288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
                                105
                                                     110
ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                      369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115
                            120
<210>
       447
<211>
       123
<212>
       PRT
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<223>
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115

Met added @ posit. 1

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Glu	Asp	Gly	Asn 20	Ile	Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Tyr 30	Asn	Ser	
His	Asn	Val 35	Tyr	Ile	Thr	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Val	
Asn	Phe 50	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly _.	Ser 60	Val	Gln	Leu	Ala	
Asp 65	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro	Asp	Asn	His	Tyr 85	Leu	Ser	Tyr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn	Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly	Ile	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
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	acc				cgc Arg											- 48
_				_	ggg Gly		_	_						_		96

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Phe Lys Ile Arg His Asn Ile 50 55	gag gac ggc agc Glu Asp Gly Ser		
cac tac cag cag aac acc ccc His Tyr Gln Gln Asn Thr Pro 65 70			
gac aac cac tac ctg agc tac Asp Asn His Tyr Leu Ser Tyr 85			
gag aag cgc gat cac atg gtc Glu Lys Arg Asp His Met Val 100			
atc act ctc ggc atg gac gag Ile Thr Leu Gly Met Asp Glu 115			366
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Asp Thr Leu Val Asn Arg Ile	10	15	
Asp Thr Leu Val Asn Arg Ile 1 5 Asp Gly Asn Ile Leu Gly His	10 Lys Leu Glu Tyr 25	Asn Tyr Asn Sen 30	r His
Asp Thr Leu Val Asn Arg Ile 5 Asp Gly Asn Ile Leu Gly His 20 Asn Val Tyr Ile Met Ala Asp	Lys Leu Glu Tyr 25 Lys Gln Lys Asn 40	Asn Tyr Asn Sen 30 Gly Ile Lys Ala 45	r His a Asn
Asp Thr Leu Val Asn Arg Ile 5 Asp Gly Asn Ile Leu Gly His 20 Asn Val Tyr Ile Met Ala Asp 35 Phe Lys Ile Arg His Asn Ile	Lys Leu Glu Tyr 25 Lys Gln Lys Asn 40 Glu Asp Gly Ser	Asn Tyr Asn Sen 30 Gly Ile Lys Ala 45 Val Gln Leu Ala 60	Asn Asp
Asp Thr Leu Val Asn Arg Ile Asp Gly Asn Ile Leu Gly His 20 Asn Val Tyr Ile Met Ala Asp 35 Phe Lys Ile Arg His Asn Ile 55 His Tyr Gln Gln Asn Thr Pro	Lys Leu Glu Tyr 25 Lys Gln Lys Asn 40 Glu Asp Gly Ser Ile Gly Asp Gly 75	Asn Tyr Asn Ser 30 Gly Ile Lys Ala 45 Val Gln Leu Ala 60 Pro Val Leu Leu	Asn Asp Pro 80

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gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc
                                                                        96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc
                                                                       144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc
                                                                       192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
                        55
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                       240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
ccc gac aac cac tac ctg age tac cag tcc gcc ctg age aaa gac ccc
                                                                       288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                       336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
                                105
                                                     110
ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                       369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala 35 40 45
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 50 55 60
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu 65 70 75 80
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro 85 90 95
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 105 110
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120
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aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35 40 45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 55 60	192
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro 65 70 75 80	240
gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn 85 90 95	288
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110	336
atc act ctc ggc atg gac gag ctg tac aag Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120	366
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Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 1. 5 10 15 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His 20 Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His 20 Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Asp Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp	
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu 15 Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His 20 Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn 35 Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp 50 His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro	

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gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
            20
                               . 25
cac aac gtc tat atc acc gcc gac aag cag aac ggc atc aag gtg
                                                                      144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
        35
                            40
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc
                                                                      192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50
                        55
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
                                                                      288
ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
                                105
                                                                      369
ggg atc act ctc ggc atg gac gag ctg tac aag
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115
                            120
<210>
       455
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and Met added @ posit. 1 <400> 455 Met Asp Thr Leu Val Asn Arg Ile (

Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1 5 10 15

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser 20 25 30

His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala 50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu 65 70 75 80

Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro 85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120

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Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1 5 10 15

96

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His 20 25 30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac 144 Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn

		35					40					45				
					aac Asn											192
					acc Thr 70											240
					agc Ser											288
					atg Met											336
					gac Asp											366
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Asp	Gly	Asn	Ile 20	Leu	Gly	His	Lys	Leu 25	Glu	Tyr	Asn	Tyr	Asn 30	Ser	His	
Asn	Val	Tyr 35	Ile	Thr	Ala	Asp	Lys 40	Gln	Lys	Asn	Gly	Ile 45	Lys	Ala	Asn	
Phe	Lys 50	Ile	Arg	His	Asn	Ile 55	Glu	Asp	Gly	Ser	Val 60	Gln	Leu	Ala	Asp	
His 65	Tyr	Gln	Gln	Asn	Thr 70	Pro	Ile	Gly	Asp	Gly 75	Pro	Val	Leu	Leu	Pro 80	
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Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc
                                                                       96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
            20
                                25
cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag qcc
                                                                      144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
        35
aac ttc aag atc cgc.cac aac atc gag gac ggc agc gtg cag ctc gcc
                                                                      192
Asn Phe Lys Ile Arq His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50
                        55
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65
ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc
                                                                      288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85
                                    90
                                                         95
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
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Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
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ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                      369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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                            120
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<223> modif. frag.; CGFP F2C, M153T, V163A, and T203Y mutations

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His	Asn	Val 35	Tyr	Ile	Thr	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Ala	
Asn	Phe 50	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Ser 60	Val	Gln	Leu	Ala	
Asp 65	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro	Asp	Asn	His	Tyr 85	Leu	Ser	Tyr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn	Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly	Ile	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
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	acc	460 ctg Leu														48
		aac Asn														96
		tat Tyr 35														144

					aac Asn											192
					acc Thr 70											240
					agc Ser											288
					atg Met											336
					gac Asp											366
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			Val	Asn 5	Arg	Ile	Glu	Leu	Lys 10	Gly	Ile	Asp	Phe	Lys 15	Glu	
Asp 1	Thr	Leu		5	Arg Gly				10	_		_		15		
Asp 1 Asp	Thr	Leu Asn	Ile 20	5 Leu		His	Lys	Leu 25	10 Glu	Tyr	Asn	Tyr	Ile 30	15 Ser	His	
Asp 1 Asp Asn	Thr Gly Val	Leu Asn Tyr 35	Ile 20	5 Leu Thr	Gly	His Asp	Lys Lys 40	Leu 25 Gln	10 Glu Lys	Tyr Asn	Asn Gly	Tyr Ile 45	Ile 30 Lys	15 Ser Ala	His Asn	
Asp 1 Asp Asn	Thr Gly Val Lys 50	Leu Asn Tyr 35	Ile 20 Ile Arg	5 Leu Thr	Gly	His Asp Ile 55	Lys Lys 40 Glu	Leu 25 Gln Asp	Glu Lys Gly	Tyr Asn Ser	Asn Gly Val 60	Tyr Ile 45 Gln	Ile 30 Lys Leu	15 Ser Ala Ala	His Asn Asp	
Asp 1 Asp Asn Phe	Thr Gly Val Lys 50	Leu Asn Tyr 35 Ile	Ile 20 Ile Arg	5 Leu Thr His	Gly Ala Asn	His Asp Ile 55	Lys Lys 40 Glu	Leu 25 Gln Asp	Glu Lys Gly Asp	Tyr Asn Ser Gly 75	Asn Gly Val 60 Pro	Tyr Ile 45 Gln Val	Ile 30 Lys Leu Leu	Ser Ala Ala Leu	His Asn Asp Pro 80	

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gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc
                                                                       96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
                                25
cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc
                                                                      144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc
                                                                      192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc
                                                                      288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                                    90
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                      336
Asn Glu Lys Arq Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
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                                                                      369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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                            120
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His	Asn	Val 35	Tyr	Ile	Thr	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Ala	
Asn	Phe 50	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Ser 60	Val	Gln	Leu	Ala	
Asp 65	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro	Asp	Asn	His	Tyr 85	Leu	Ser	Tyr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn	Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly	Ile	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
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	acc	164 ctg Leu														48
		aac Asn														96

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35	•	40	45
		gag gac ggc agc gtg Glu Asp Gly Ser Val 60	
		atc ggc gac ggc ccc Ile Gly Asp Gly Pro 75	
		cag tcc gcc ctg agc Gln Ser Ala Leu Ser 90	
		ctg ctg gag ttc gtg Leu Leu Glu Phe Val 105	
atc act ctc ggc Ile Thr Leu Gly 115	Met Asp Glu		366
<210> 465 <211> 122 <212> PRT <213> Artificia	al		
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	rag.; BFP F2C	w. Y145F mutation	
	rag.; BFP F2C	w. Y145F mutation	
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<223> modif. f: <400> 465 Asp Thr Leu Val	Asn Arg Ile (Glu Leu Lys Gly Ile	15
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<223> modif. for the second se	Asn Arg Ile (5) Leu Gly His I	Glu Leu Lys Gly Ile 10 Lys Leu Glu Tyr Asn 25 Lys Gln Lys Asn Gly	Phe Asn Ser His 30 Ile Lys Val Asn 45
<223> modif. for control of the cont	Asn Arg Ile (5) Leu Gly His I Met Ala Asp I His Asn Ile (5)	Glu Leu Lys Gly Ile 10 Lys Leu Glu Tyr Asn 25 Lys Gln Lys Asn Gly 40	Phe Asn Ser His 30 Ile Lys Val Asn 45 Gln Leu Ala Asp

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly 100 105 110

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115
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gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc
                                                                       96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser
            20
cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg
                                                                       144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
        35
aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc
                                                                      192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
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                        55
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                       240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65
                                         75
ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc
                                                                       288
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
                85
                                                         95
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
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                                105
                                                     110
                                                                      369
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Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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His	Asn	Val 35	Tyr	Ile	Met	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Val	
Asn	Phe 50	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Ser 60	Val	Gln	Leu	Ala	
Asp 65	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro	Asp	Asn	His	Tyr 85	Leu	Ser	Thr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn	Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly	Ile	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
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					ggg Gly											96

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Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn

		35					40					45				
					aac Asn											192
					acc Thr 70											240
					agc Ser											288
					atg Met											336
					gac Asp											366
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Asn	Val	Tyr 35	Ile	Met	Ala	Asp	Lys 40	Gln	Lys	Asn	Gly	Ile 45	Lys	Val	Asn	
Phe	Lys 50	Ile	Arg	His	Asn	Ile 55	Glu	Asp	Gly	Gly	Val 60	Gln	Leu	Ala	Asp	
His 65	Tyr	Gln	Gln	Asn	Thr 70	Pro	Ile	Gly	Asp	Gly 75	Pro	Val	Leu	Leu	Pro 80	
Asp	Asn	His	Tyr	Leu 85	Ser	Tyr	Gln	Ser	Ala 90	Leu	Ser	Lys	Asp	Pro 95	Asn	
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115
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Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc
                                                                      96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
            20
                                25
cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg
                                                                     144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
        35
                            40
aac ttc aag atc cgc cac aac atc gag gac ggc gtg cag ctc gcc
                                                                     192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                     240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
                    70
ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc
                                                                     288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc qcc gcc
                                                                     336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
           100
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ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                     369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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Glu	Asp	Gly	Asn 20	Ile	Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Tyr 30	Asn	Ser	
His	Asn	Val 35	Tyr	Ile	Met	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Val	
Asn	Phe 50	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Gly 60	Val	Gln	Leu	Ala	
Asp 65	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro	Asp	Asn	His	Tyr 85	Leu	Ser	Tyr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn	Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly	Ile	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
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	acc				cgc Arg											48
					ggg Gly											96

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Phe I	aag Lys 50	atc Ile	cgc Arg	cac His	aac Asn	atc Ile 55	gag Glu	gac Asp	ggc Gly	ggc Gly	gtg Val 60	cag Gln	ctc Leu	gcc Ala	gac Asp	192
cac t His T 65																240
gac a Asp A																288
gag a Glu L																336
atc a Ile T				_	_		_		_							366
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Asp T			Val	Asn _. 5	Arg	Ile	Glu	Leu	Lys 10	Gly	Ile	Asp	Phe	Lys 15	Glu	
Asp T	Γhr	Leu		5					10			_		15		
Asp I	Thr 3ly	Leu Asn	Ile 20	5 Leu	Gly	His	Lys	Leu 25	10 Glu	Tyr	Asn	Tyr	Asn 30	15 Ser	His	
Asp G Asp V Phe L	Thr Gly Val	Leu Asn Tyr 35	Ile 20	5 Leu Thr	Gly Ala	His Asp	Lys Lys 40	Leu 25 Gln	10 Glu Lys	Tyr Asn	Asn Gly	Tyr Ile 45	Asn 30 Lys	15 Ser Val	His Asn	
Asp G Asp V Phe L	Thr Gly Val	Leu Asn Tyr 35	Ile 20 Ile Arg	5 Leu Thr	Gly Ala Asn	His Asp Ile 55	Lys Lys 40 Glu	Leu 25 Gln Asp	Glu Lys Gly	Tyr Asn Gly	Asn Gly Val 60	Tyr Ile 45 Gln	Asn 30 Lys Leu	15 Ser Val	His Asn Asp	
Asp G Asn V Phe L His T	Thr Gly Val	Leu Asn Tyr 35 Ile	Ile 20 Ile Arg Gln	5 Leu Thr His	Gly Ala Asn Thr	His Asp Ile 55	Lys Lys 40 Glu	Leu 25 Gln Asp	Glu Lys Gly Asp	Tyr Asn Gly Gly 75	Asn Gly Val 60	Tyr Ile 45 Gln Val	Asn 30 Lys Leu Leu	Ser Val Ala	His Asn Asp Pro 80	

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gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc
                                                                       96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg
                                                                      144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc
                                                                      192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala
                        55
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
                                        75
ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc
                                                                      288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85
aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
                                105
                                                     110
ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                      369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115
                            120
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Glu A	Asp	Gly	Asn 20	Ile	Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Tyr 30	Asn	Ser	
His A	Asn	Val 35	Tyr	Ile	Thr	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Val	
Asn I	Phe	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Gly 60	Val	Gln	Leu	Ala	
Asp H	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro A	Asp	Asn	His	Tyr 85	Leu	Ser	Tyr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn (Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly 1	lle	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
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144

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Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn

25

20

	Lys 50				aac Asn											192
	tac Tyr															240
	aac Asn															288
	aag Lys															336
	act Thr															366
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	Thr		Val	Asn 5	Arg	Ile	Glu	Leu	Lys 10	Gly	Ile	Asp	Phe	Lys 15	Glu	
Asp 1		Leu		5	_				10			_		15		
Asp 1	Thr	Leu Asn	Ile 20	5 Leu	Gly	His	Lys	Leu 25	10 Glu	Tyr	Asn	Tyr	Asn 30	15 Ser	His	
Asp 1 Asp	Thr	Leu Asn Tyr 35	Ile 20	5 Leu Met	Gly	His Asp	Lys Lys 40	Leu 25 Gln	10 Glu Lys	Tyr Asn	Asn Gly	Tyr Ile 45	Asn 30 Lys	15 Ser Ala	His Asn	
Asp Asp Asn	Thr Gly Val	Leu Asn Tyr 35	Ile 20 Ile Arg	5 Leu Met	Gly Ala Asn	His Asp Ile 55	Lys Lys 40 Glu	Leu 25 Gln Asp	10 Glu Lys Gly	Tyr Asn Gly	Asn Gly Val 60	Tyr Ile 45 Gln	Asn 30 Lys Leu	15 Ser Ala Ala	His Asn Asp	
Asp Asp Asn Phe	Thr Gly Val Lys 50	Leu Asn Tyr 35 Ile	Ile 20 Ile Arg	Leu Met His	Gly Ala Asn Thr	His Asp Ile 55	Lys Lys 40 Glu	Leu 25 Gln Asp	Glu Lys Gly Asp	Tyr Asn Gly Gly 75	Asn Gly Val 60	Tyr Ile 45 Gln Val	Asn 30 Lys Leu Leu	15 Ser Ala Ala	His Asn Asp Pro 80	

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Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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<210> 478
<211>
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gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc
                                                                       96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
                                25
cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc
                                                                      144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
                            40
aac ttc aag atc cgc cac aac atc gag gac ggc gtg cag ctc gcc
                                                                      192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                     240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc
                                                                     288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
aac gag aag cgc gat cac atg gtc ctg ctq qaq ttc gtq acc gcc qcc
                                                                     336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100
                                105
ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                     369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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Glu	Asp	Gly	Asn 20	Ile	Leu	Gly	His	Lys 25	Leu	Glu	Tyr	Asn	Tyr 30	Asn	Ser	
His	Asn	Val 35	Tyr	Ile	Met	Ala	Asp 40	Lys	Gln	Lys	Asn	Gly 45	Ile	Lys	Ala	
Asn	Phe 50	Lys	Ile	Arg	His	Asn 55	Ile	Glu	Asp	Gly	Gly 60	Val	Gln	Leu	Ala	
Asp 65	His	Tyr	Gln	Gln	Asn 70	Thr	Pro	Ile	Gly	Asp 75	Gly	Pro	Val	Leu	Leu 80	
Pro	Asp	Asn	His	Tyr 85	Leu	Ser	Tyr	Gln	Ser 90	Ala	Leu	Ser	Lys	Asp 95	Pro	
Asn	Glu	Lys	Arg 100	Asp	His	Met	Val	Leu 105	Leu	Glu	Phe	Val	Thr 110	Ala	Ala	
Gly	Ile	Thr 115	Leu	Gly	Met	Asp	Glu 120	Leu	Tyr	Lys						
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					ggg Gly											96
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cac tac cag His Tyr Gl 65													240
gac aac ca Asp Asn Hi		u Ser											288
gag aag cg Glu Lys Arg													336
atc act cto Ile Thr Let 11!	ı Gly Me												366
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Asp Thr Let	5					10					15		
Asp Thr Let	5 n Ile Le 20	u Gly	His	Lys ·	Leu 25	10 Glu	Tyr	Asn	Tyr	Asn 30	15 Ser	His	
Asp Gly Ass	5 i Ile Le 20 The Th	u Gly r Ala	His Asp	Lys Lys 40	Leu 25 Gln	10 Glu Lys	Tyr Asn	Asn Gly	Tyr Ile 45	Asn 30 Lys	15 Ser Ala	His Asn	
Asp Thr Lendal Asp Gly Assa Val Tyr 35	5 I lle Le 20 The The	r Ala	His Asp Ile 55	Lys Lys 40	Leu 25 Gln Asp	Glu Lys	Tyr Asn Gly	Asn Gly Val 60	Tyr Ile 45 Gln	Asn 30 Lys Leu	Ser Ala Ala	His Asn Asp	7
Asp Thr Length 1 Asp Gly Asi Asn Val Tyr 35 Phe Lys Ile 50 His Tyr Gli	5 Ile Le 20 The Arg Hi	eu Gly or Ala s Asn on Thr 70 ou Ser	His Asp Ile 55	Lys Lys 40 Glu	Leu 25 Gln Asp	10 Glu Lys Gly Asp	Tyr Asn Gly Gly 75	Asn Gly Val 60 Pro	Tyr Ile 45 Gln Val	Asn 30 Lys Leu Leu	Ser Ala Ala Leu	His Asn Asp Pro 80	

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Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc
                                                                         96
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
 cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc
                                                                        144
 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
         35
                                                  45
 aac ttc aag atc cgc cac aac atc gag gac ggc gtg cag ctc gcc
                                                                        192
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Val Gln Leu Ala
     50
                          55
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg
                                                                        240
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 65
                                          75
 ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc
                                                                        288
 Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                 85
                                                          95
 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc
                                                                        336
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
             100
                                  105
                                                      110
 ggg atc act ctc ggc atg gac gag ctg tac aag
                                                                        369
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser 20 25 30

His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala 35 40 45

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala 50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu 65 70 75 80

Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro 85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala 100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys 115 120

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<211> 471

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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144

_	Glu	Gly 35	Asp	Ala	Thr	Tyr	Gly 40	Lys	Leu	Thr	Leu	Lys 45	Phe	Ile	Cys	
					ccc Pro											192
					tgc Cys 70											240
					tcc Ser											288
					gac Asp											336
					acc Thr											384
					ggc Gly											432
					gtc Val 150											471
<210 <211 <211 <211	l> : 2> :	185 157 PRT Artif	icia	al												
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<213 <213 <213 <220	1 > 2 1 3 2 1 3 2 1 3 2 1 3 2 1 3 3 3 1 3 3 3 3 3	157 PRT Artif	_		. YFI	? F1I	OX w.	. pos	sitio	on 1	Met	remo	oved			
<211 <211 <211 <221 <221 <400	1> 1 2> 1 3> 1 0> 2 3> r	157 PRT Artif Modif	E. fi	rag.;	: YFI Glu			-						Leu 15	Val	
<21: <21: <21: <22: <40: Val	1> 1 2> 1 3> 1 0> 3 3> r Ser	L57 PRT Artif modif L85 Lys	f. fi	rag.; Glu 5		Leu	Phe	Thr	Gly 10	Val	Val	Pro	Ile	15		
<21: <21: <21: <22: <40: Val Glu	1> : 2> I 3> / 3> / 3> / 0> Ser	L57 PRT Artif Modif L85 Lys	Gly Gly 20	Glu 5 Asp	Glu	Leu Asn	Phe Gly	Thr His	Gly 10 Lys	Val Phe	Val Ser	Pro Val	Ile Ser 30	15 Gly	Glu	
<21: <21: <22: <22: <40: Val 1 Glu Gly	1 > : : : : : : : : : : : : : : : : : :	Asp Gly 35	Gly Gly 20 Asp	Glu 5 Asp	Glu Val	Leu Asn Tyr	Phe Gly Gly 40	Thr His 25	Gly 10 Lys Leu	Val Phe Thr	Val Ser Leu	Pro Val Lys 45	Ile Ser 30	15 Gly Ile	Glu Cys	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 120 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 150 <210> 486 <211> 474 <212> DNA <213> Artificial <220> modif. frag.; YFP F1DX with K79R mutation <223> <220> <221> CDS <222> (1)..(474) <400> 486 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 tto ggc tac ggc ctg cag tgc tto gcc cgc tac ccc gac cac atg aag 240 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 80 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100	105	110	
gtg aag ttc gag ggc ga Val Lys Phe Glu Gly A 115			
atc gac ttc aag gag galle Asp Phe Lys Glu As			
aac tac aac agc cac a Asn Tyr Asn Ser His A 145	sn Val Tyr Ile Met A		474
<210> 487 <211> 158 <212> PRT <213> Artificial			
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Val Glu Leu Asp Gly As 20	sp Val Asn Gly His I 25	Lys Phe Ser Val Ser 30	Gly
Glu Gly Glu Gly Asp A	a Thr Tyr Gly Lys I	Leu Thr Leu Lys Phe 45	Ile
Cys Thr Thr Gly Lys Lo	eu Pro Val Pro Trp I 55	Pro Thr Leu Val Thr 60	Thr
Phe Gly Tyr Gly Leu G	_	Tyr Pro Asp His Met 75	Lys 80
Arg His Asp Phe Phe Ly	s Ser Ala Met Pro (90	Glu Gly Tyr Val Gln 95	Glu
Arg Thr Ile Phe Phe Ly	s Asp Asp Gly Asn 1	Tyr Lys Thr Arg Ala 110	Glu
Val Lys Phe Glu Gly As	sp Thr Leu Val Asn A	Arg Ile Glu Leu Lys 125	Gly
Ile Asp Phe Lys Glu As	sp Gly Asn Ile Leu (135	Gly His Lys Leu Glu 140	Tyr

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Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln

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<220>
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<400> 489
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<211> 157

<213> Artificial

<223> modif. frag.; YFP F1DX, w. K79R mutation, and posit. 1 Met

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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 40

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 70

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 135

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 150

<210> 490

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1DX with Y66F mutation

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<222> (1)..(474)
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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
                                                                       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
                                                                      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
                                                                      240
Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                    70
egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag
                                                                      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag
                                                                      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
                                                                      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
                            120
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac
                                                                      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
                        135
                                                                      474
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
<210> 491
<211> 158
<212> PRT
<213> Artificial
<220>
      modif. frag.; YFP F1DX with Y66F mutation
<400> 491
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 55 Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 75 70 80 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Glu Glu 85 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 105 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 120 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 . Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 150 <210> 492 <211> 471 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F1DX, Y66F mutation, and posit. 1 Met removed <220> <221> CDS (1)..(471) <222> <400> 492 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 10 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc qag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu ggc gag ggc gat gcc acc tac ggc aag ctq acc ctq aaq ttc atc tqc 144 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 60	192
ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
tac aac agc cac aac gtc tat atc atg gcc gac aag cag Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155	471
<210> 493 <211> 157	
<212> PRT <213> Artificial	
	e d
<213> Artificial <220>	e d
<220> <223> modif. frag.; YFP F1DX, Y66F mutation, and posit. 1 Met remove	ed
<220> <223> modif. frag.; YFP F1DX, Y66F mutation, and posit. 1 Met remove <400> 493 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	ed
<220> <223> modif. frag.; YFP F1DX, Y66F mutation, and posit. 1 Met remove <400> 493 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	ed
<pre><213> Artificial <220> <223> modif. frag.; YFP F1DX, Y66F mutation, and posit. 1 Met remove <400> 493 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1</pre>	ed

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arq 85 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 135 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 150 <210> 494 <211> 474 <212> DNA <213> Artificial <220> <223> modif. frag.; YFP F1DX with Q69K mutation <220> <221> CDS <222> (1)..(474) <400> 494 atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc qgc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 tto ggo tac ggo ctg aag tgo tto goo cgo tac ccc gac cac atg aag 240 Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 75 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu cgc acc atc ttc ttc aag gac ggc aac tac aag acc cgc gcc gag 336

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100)	105	110
		gtg aac cgc atc gag Val Asn Arg Ile Glu 125	
		atc ctg ggg cac aag Ile Leu Gly His Lys 140	
		atc atg gcc gac aag Ile Met Ala Asp Lys 155	
<210> 495 <211> 158 <212> PRT <213> Artifici	al		
<220> <223> modif. f	rag.; YFP F1DX wi	th Q69K mutation	
<400> 495			
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Val Glu Leu Asp 20	o Gly Asp Val Asn	Gly His Lys Phe Ser 25	Val Ser Gly 30
Glu Gly Glu Gly 35	Asp Ala Thr Tyr	Gly Lys Leu Thr Leu 45	Lys Phe Ile
Cys Thr Thr Gly	/ Lys Leu Pro Val 55	Pro Trp Pro Thr Leu 60	Val Thr Thr
Phe Gly Tyr Gly 65	Leu Lys Cys Phe	Ala Arg Tyr Pro Asp 75	His Met Lys 80
Arg His Asp Phe	e Phe Lys Ser Ala 85	Met Pro Glu Gly Tyr 90	Val Gln Glu 95
Arg Thr Ile Phe		Gly Asn Tyr Lys Thr 105	Arg Ala Glu 110
Val Lys Phe Glu	Gly Asp Thr Leu 120	Val Asn Arg Ile Glu 125	Leu Lys Gly
Ile Asp Phe Lys	Glu Asp Gly Asn 135	Ile Leu Gly His Lys 140	Leu Glu Tyr

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155
<210> 496 <211> 471 <212> DNA <213> Artificial
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gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60
ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140
tac aac agc cac aac gtc tat atc atg gcc gac aag cag Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155

<211> 157

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1DX, Q69K mutation, and posit. 1 Met removed

<400> 497

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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60

Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155

<210> 498

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; citrine F1DX with V68L, Q69M mutations

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<221>
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       (1)...(474)
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
                                                                       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                25
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
                                                                      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50
tto ggo tac ggo ctg atg tgo tto gcc cgc tac ccc gac cac atg aag
                                                                      240
Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                    70
egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag
                                                                      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
ege ace ate the the aag gae gae gge aac tae aag ace ege gee gag
                                                                      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100
                                105
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
                                                                      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115
                            120
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac
                                                                      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130
                        135
                                                                      474
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
<210>
      499
<211>
      158
<212>
       PRT
<213>
      Artificial
<220>
<223>
      modif. frag.; citrine F1DX with V68L, Q69M mutations
<400> 499
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                5
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 40 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 55 Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys 70 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 150 <210> 500 <211> 471 <212> DNA <213> Artificial <220> <223> modif. frag.; citrine F1DX, V68L and Q69M mutations, and position 1 Met removed <220> <221> CDS <222> (1)..(471) <400> 500 gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg gtc 48 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 5 10 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25

ggc gag gg Gly Glu Gl 35				_			_	144
acc acc gg Thr Thr Gl 50								192
ggc tac gg Gly Tyr Gl 65								240
cac gac tt His Asp Ph							u Arg	288
acc atc tt Thr Ile Ph				Tyr Lys				336
aag ttc ga Lys Phe Gl 11	u Gly Asp							384
gac ttc aa Asp Phe Ly 130								432
tac aac ag Tyr Asn Se 145								471
<210> 501 <211> 157 <212> PRT <213> Art	ificial							
	if. frag. position			V68L an	d Q69M m	utation	S,	
<400> 501								
Val Ser Ly 1	s Gly Glu 5	Glu Leu	Phe Thr	Gly Val 10	Val Pro	Ile Le 15		
Glu Leu As	p Gly Asp 20	Val Asn	Gly His 25	Lys Phe	Ser Val	Ser Gl 30	y Glu	
Gly Glu Gl	y Asp Ala	Thr Tyr	Gly Lys 40	Leu Thr	Leu Lys 45	Phe Il	e Cys	
Thr Thr Gl 50	y Lys Leu	Pro Val	Pro Trp	Pro Thr	Leu Val	Thr Th	r Phe	

Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155	
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-220	
<220> <223> modif. frag.; CFP F1DX with F64L mutation	
<223> modif. frag.; CFP F1DX with F64L mutation <220> <221> CDS <222> (1)(474) <400> 502	:8
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<pre><223> modif. frag.; CFP F1DX with F64L mutation <220> <221> CDS <222> (1)(474) <400> 502 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu 1</pre>	6
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	ggc gac acc ctg gtg Gly Asp Thr Leu Val 120		
	gag gac ggc aac atc Glu Asp Gly Asn Ile 135		
	cac aac gtc tat atc His Asn Val Tyr Ile 150		474
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Glu Gly Glu Gly 35	25 Asp Ala Thr Tyr Gly	Lys Leu Thr Leu Lys 45	Phe Ile
Glu Gly Glu Gly 35 Cys Thr Thr Gly 50	Asp Ala Thr Tyr Gly 40 Lys Leu Pro Val Pro	Lys Leu Thr Leu Lys 45 Trp Pro Thr Leu Val 60	Phe Ile Thr Thr

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140

Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln
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ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 55 60	192
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
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145 150 155

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
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Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
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Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
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Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
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Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145
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      506
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      DNA
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Glu	Gly	Glu 35	Gly	Asp	Ala	Thr	Tyr 40	Gly	Lys	Leu	Thr	Leu 45	Lys	Phe	Ile	
Cys	Thr 50	Thr	Gly	Lys	Leu	Pro 55	Val	Pro	Trp	Pro	Thr 60	Leu	Val	Thr	Thr	
Leu 65	Thr	Trp	Gly	Leu	Gln 70	Cys	Phe	Ala	Arg	Tyr 75	Pro	Asp	His	Met	Lys 80	
Arg	His	Asp	Phe	Phe 85	Lys	Ser	Ala	Met	Pro 90	Glu	Gly	Tyr	Val	Gln 95	Glu	
Arg	Thr	Ile	Phe 100	Phe	Lys	Asp	Asp	Gly 105	Asn	Tyr	Lys	Thr	Arg 110	Ala	Glu	
Val	Lys	Phe 115	Glu	Gly	Asp	Thr	Leu 120	Val	Asn	Arg	Ile	Glu 125	Leu	Lys	Gly	
Ile	Asp 130	Phe	Lys	Glu	Asp	Gly 135	Asn	Ile	Leu	Gly	His 140	Lys	Leu	Glu	Tyr	
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					gta Val											96
aac	gag	aac	gat.	acc	acc	tac	ggc	ааσ	cta	acc	cta	ааσ	ttc	atc	tac	144

Gly	Glu	Gly 35	Asp	Ala	Thr	Tyr	Gly 40	Lys	Leu	Thr	Leu	Lys 45	Phe	Ile	Cys	
					ccc Pro											192
					tgc Cys 70											240
					tcc Ser											288
					gac Asp											336
					acc Thr											384
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					gtc Val 150											471
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65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 135 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 150 <210> 510 <211> 474 <212> DNA <213> Artificial <223> modif. frag.; CFP F1DX with Y66W mutation <220> <221> CDS <222> (1)..(474) <400> 510 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 tte gge tgg gge etg eag tge tte gee ege tae eee gae eae atg aag 240 Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 egg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100	105	110
gtg aag ttc gag ggc gac Val Lys Phe Glu Gly Asp 115		
atc gac ttc aag gag gac Ile Asp Phe Lys Glu Asp 130	Gly Asn Ile Leu Gly H	
aac tac aac agc cac aac Asn Tyr Asn Ser His Asn 145	Val Tyr Ile Met Ala A	
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Val Glu Leu Asp Gly Asp 20	Val Asn Gly His Lys P 25	Phe Ser Val Ser Gly
Glu Gly Glu Gly Asp Ala	Thr Tyr Gly Lys Leu T	hr Leu Lys Phe Ile 45
Cys Thr Thr Gly Lys Leu 50	_	Thr Leu Val Thr Thr
Phe Gly Trp Gly Leu Gln	Cys Phe Ala Arg Tyr P 75	Pro Asp His Met Lys 80
Arg His Asp Phe Phe Lys	Ser Ala Met Pro Glu G 90	ly Tyr Val Gln Glu 95
Arg Thr Ile Phe Phe Lys	Asp Asp Gly Asn Tyr L	ys Thr Arg Ala Glu 110
Val Lys Phe Glu Gly Asp 115	Thr Leu Val Asn Arg I	le Glu Leu Lys Gly 125
Ile Asp Phe Lys Glu Asp		is Lys Leu Glu Tyr 40

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Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                            40
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50
                        55
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
                    70
                                        75
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130
                        135
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145
                    150
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                                                                       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
                                 25
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
                                                                      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
                        55
tto ggc tgg ggc ctg cag tgc tto gcc cgc tac ccc gac cac atg aaq
                                                                      240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
                                                                      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag
                                                                      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100
                                105
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
                                                                      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115
                            120
atc gad ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac
                                                                      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130
                        135
aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag
                                                                      474
Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys
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      PRT
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                5
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

:0	25	30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125

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Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys 145 150 155

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<212> DNA

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 posit. 1 Met removed

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ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

48

96

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
tac atc agc cac aac gtc tat atc atg gcc gac aag cag Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155	471
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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 135 Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln <210> 518 <211> 474 <212> DNA <213> Artificial <220> modif. frag.; CFP F1DX w. Y66W, M153T mutations <223> <220> <221> CDS <222> (1)...(474)<400> 518 atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240 Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 70 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 90 ege ace ate the the aag gae gae gge aac tae aag ace ege gee gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100		105	110	
	Gly Asp Thr L	ctg gtg aac cgc a Leu Val Asn Arg 120		
atc gac ttc aag Ile Asp Phe Lys 130	gag gac ggc a Glu Asp Gly A 135	aac atc ctg ggg (Asn Ile Leu Gly 1	cac aag ctg gag His Lys Leu Glu 140	tac 432 Tyr
		at atc acc gcc grant atc acc gcc gcc grant atc acc gcc gcc grant atc acc gcc gcc gcc gcc gcc gcc gcc gcc gc		474
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Val Glu Leu Asp 20	Gly Asp Val A	asn Gly His Lys	Phe Ser Val Ser 30	Gly
Glu Gly Glu Gly 35	•	Tyr Gly Lys Leu : :0	Thr Leu Lys Phe 45	Ile
Cys Thr Thr Gly 50	Lys Leu Pro V	al Pro Trp Pro :	Thr Leu Val Thr 60	Thr
Phe Gly Trp Gly 65	Leu Gln Cys P	Phe Ala Arg Tyr 1 75	Pro Asp His Met	Lys 80
Arg His Asp Phe	Phe Lys Ser A	ala Met Pro Glu (90	Gly Tyr Val Gln 95	Glu
Arg Thr Ile Phe	Phe Lys Asp A	sp Gly Asn Tyr 1 105	Lys Thr Arg Ala 110	Glu

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

145				150		-2-			155		-1-					
<210><211><211><212><213>	520 471 DNA Arti	fici	al													
<220> <223>	modi posi					DX w	. Y60	6W, I	M153'	Ր տա	tatio	ons,	and			
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gag ct Glu Le																96
ggc ga Gly Gl																144
acc ac Thr Th 50																192
ggc tg Gly Tr 65																240
cac ga His As																288
acc at Thr Il	c ttc e Phe	ttc Phe 100	aag Lys	gac Asp	gac Asp	ggc Gly	aac Asn 105	tac Tyr	aag Lys	acc Thr	cgc Arg	gcc Ala 110	gag Glu	gtg Val		336
aag tt Lys Ph	c gag e Glu 115	ggc Gly	gac Asp	acc Thr	ctg Leu	gtg Val 120	aac Asn	cgc Arg	atc Ile	gag Glu	ctg Leu 125	aag Lys	ggc Gly	atc Ile		384
gac tt Asp Ph	e Lys															432
tac aa Tyr As: 145																471

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln

<210> 521

<211> 157

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1DX w. Y66W, M153T mutations, and
 posit. 1 Met removed

<400> 521

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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln 145 150 155

<210> 522

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1DX with N146I mutation

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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
                                                                       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc
                                                                      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
                                                                      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
egg cac gae the the aag tee gee atg eee gaa gge tae gte eag gag
                                                                      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
ege ace ate the the aag gae gae gge aac tae aag ace ege gee gag
                                                                      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
                                105
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
                                                                      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
                            120
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac
                                                                      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
                        135
aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag
                                                                      474
Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
                    150
<210> 523
<211> 158
<212> PRT
<213> Artificial
<220>
      modif. frag.; CFP F1DX with N146I mutation
<400> 523
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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20 25 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 55 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 70 75 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140 Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 150 <210> 524 <211> 471 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F1DX w. N146I mutation, and posit. 1 Met removed <220> <221> CDS <222> (1)..(471) <400> 524 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 10 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val 50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His 65 70 75	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val 85 90	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg 100 105	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu 115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu 130 135 140	
tac atc agc cac aac gtc tat atc atg gcc gac aag cag Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 145 150 155	471
<210> 525 <211> 157 <212> PRT <213> Artificial	
<220> <223> modif. frag.; CFP F1DX w. N146I mutation, and removed	posit. 1 Met
<400> 525	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro 1 5 10	Ile Leu Val 15
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro 1 5 10 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val	15
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro 1 5 10 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val	15 Ser Gly Glu 30
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro 1 5 10 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val 20 25 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys	Ser Gly Glu 30 Phe Ile Cys

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 105 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 120 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 135 Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 150 <210> 526 <211> 474 <212> DNA <213> Artificial <220> modif. frag.; CFP F1DX with M153T mutation <223> <220> <221> CDS <222> (1)..(474) <400> 526 atg gtg agc aag ggc gag gtg ttc acc ggg gtg gtg ccc atc ctg 48 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 65 egg cae gae tte tte aag tee gee atg eee gaa gge tae gte eag gag 288 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Glu Glu 85 ege ace ate the the aag gae gae gge aac tae aag ace ege gee gag 336 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100	105	110

								gtg Val								384
								atc Ile								432
								atc Ile								474
<210 <211 <212 <213	.> : !> !	527 158 PRT Artii	ficia	al		·										
<220 <223		nodi	E. fi	rag.	; CFI	P F1I	OX w:	ith N	11537	r mut	tatio	on				
<400)> 5	527														
Met 1	Val	Ser	Lys	Gly 5	Glu	Glu	Leu	Phe	Thr 10	Gly	Val	Val	Pro	Ile 15	Leu	
Val	Glu	Leu	Asp 20	Gly	Asp	Val	Asn	Gly 25	His	Lys	Phe	Ser	Val 30	Ser	Gly	
Glu	Gly	Glu 35	Gly	Asp	Ala	Thr	Tyr 40	Gly	Lys	Leu	Thr	Leu 45	Lys	Phe	Ile	
_	Thr 50	Thr	Gly	Lys	Leu	Pro 55	Val	Pro	Trp	Pro	Thr 60	Leu	Val	Thr	Thr	
Phe 65	Gly	Tyr	Gly	Leu	Gln 70	Cys	Phe	Ala	Arg	Tyr 75	Pro	Asp	His	Met	Lys 80	
Arg	His	Asp	Phe	Phe 85	Lys	Ser	Ala	Met	Pro 90	Glu	Gly	Tyr	Val	Gln 95	Glu	
Arg	Thr	Ile	Phe 100	Phe	Lys	Asp	Asp	Gly 105	Asn	Tyr	Lys	Thr	Arg 110	Ala	Glu	
Val	Lys	Phe 115	Glu	Gly	Asp	Thr	Leu 120	Val	Asn	Arg	Ile	Glu 125	Leu	Lys	Gly	
Ile	Asp 130	Phe	Lys	Glu	Asp	Gly 135	Asn	Ile	Leu	Gly	His 140	Lys	Leu	Glu	Tyr	

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln 145 150 155	
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gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
tac aac agc cac aac gtc tat atc acc gcc gac aag cag Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln 145 150 155	471

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<210> 529
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        Met removed
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 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
                                 25
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                            40
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                 85
                                     90
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
             100
                                 105
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
                             120
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
     130
                         135
 Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145
                     150
 <210> 530
 <211> 474
 <212> DNA
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<223> modif. frag.; CFP F1DX w. N146I, M153T mutations

<213> Artificial

<220>

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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc
                                                                      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aaq ttc atc
                                                                     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc
                                                                     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag
                                                                     240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
                    70
egg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag
                                                                     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
ege ace ate tte tte aag gae gge aac tae aag ace ege gee gag
                                                                     336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
                                105
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc
                                                                     384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
                            120
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac
                                                                     432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
                        135
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag
                                                                     474
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
<210> 531
<211> 158
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      modif. frag.; CFP F1DX w. N146I, M153T mutations
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly 20 25 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile 35 40 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr 50 55 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys 75 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu 85 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 120 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 135 Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln 150 <210> 532 <211> 471 <212> DNA <213> Artificial <220> <223> modif. frag.; CFP F1DX, N146I, M153T mutations, and posit. 1 Met removed <220> <221> CDS <222> (1)..(471) <400> 532 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 15 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tqc 144 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60	192
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
tac atc agc cac aac gtc tat atc acc gcc gac aag cag Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln 145 150 155	471
<210> 533 <211> 157 <212> PRT <213> Artificial	
<220> <223> modif. frag.; CFP F1DX, N146I, M153T mutations, and posit. 1 Met removed	
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 15 Clu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 Phe Ile Cys	

His	Asp	Phe	Phe	Lys 85	Ser	Ala	Met	Pro	Glu 90	Gly	Tyr	Val	Gln	Glu 95	Arg		
Thr	Ile	Phe	Phe 100	Lys	Asp	Asp	Gly	Asn 105	Tyr	Lys	Thr	Arg	Ala 110	Glu	Val		
Lys	Phe	Glu 115	Gly	Asp	Thr	Leu	Val 120	Asn	Arg	Ile	Glu	Leu 125	Lys	Gly	Ile		
Asp	Phe 130	Lys	Glu	Asp	Gly	Asn 135	Ile	Leu	Gly	His	Lys 140	Leu	Glu	Tyr	Asn		
Tyr 145	Ile	Ser	His	Asn	Val 150	Tyr	Ile	Thr	Ala	Asp 155	Lys	Gln					
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	gtg							ttc Phe									48
atg Met 1 gtc	gtg Val gag	agc Ser	Lys	Gly 5 ggc	Glu gac	Glu gta	Leu aac		Thr 10 cac	Gly aag	Val ttc	Val	Pro gtg	Ile 15 tcc	Leu		48 96
atg Met 1 gtc Val	gtg Val gag Glu	agc Ser ctg Leu	gac Asp 20	Gly 5 ggc Gly gat	Glu gac Asp gcc	Glu gta Val acc	Leu aac Asn tac	Phe ggc Gly	Thr 10 cac His	Gly aag Lys ctg	Val ttc Phe acc	val agc Ser	Pro gtg Val 30	Ile 15 tcc Ser	ggc Gly		
atg Met 1 gtc Val gag Glu	gtg Val gag Glu ggc Gly acc	agc Ser Ctg Leu gag Glu 35	Lys gac Asp 20 ggc Gly	Gly 5 ggc Gly gat Asp	Glu gac Asp gcc Ala	Glu gta Val acc Thr	Leu aac Asn tac Tyr 40	ggc Gly 25	Thr 10 cac His aag Lys	aag Lys ctg Leu ccc Pro	Val ttc Phe acc Thr	Val agc Ser ctg Leu 45	Pro gtg Val 30 aag Lys	lle 15 tcc ser ttc Phe	Leu ggc Gly atc Ile		96
atg Met 1 gtc Val gag Glu tgc Cys	gag Glu ggc Gly acc Thr 50	agc Ser ctg Leu gag Glu 35 acc Thr	Lys gac Asp 20 ggc Gly ggc Gly	Gly 5 ggc Gly gat Asp aag Lys	gac Asp gcc Ala ctg Leu	gta Val acc Thr	Leu aac Asn tac Tyr 40 gtg Val	ggc Gly 25 ggc Gly	Thr 10 cac His aag Lys tgg Trp	aag Lys ctg Leu ccc Pro	Val ttc Phe acc Thr acc Thr 60 ccc	val agc ser ctg Leu 45 ctc Leu gac	gtg Val 30 aag Lys gtg Val	Ile 15 tcc Ser ttc Phe acc Thr	ggc Gly atc Ile acc Thr	:	96 144
atg Met 1 gtc Val gag Glu tgc Cys ttc Phe 65 cgg	gag Glu ggc Gly acc Thr 50 ggc Gly	agc Ser ctg Leu gag Glu 35 acc Thr tgg Trp	Lys gac Asp 20 ggc Gly ggc Gly ttc	Gly 5 ggc Gly gat Asp aag Lys ctg Leu	Glu gac Asp gcc Ala ctg Leu cag Gln 70 aag	Glu gta Val acc Thr ccc Pro 55 tgc Cys	Leu aac Asn tac Tyr 40 gtg Val ttc Phe	Phe ggc Gly 25 ggc Gly ccc Pro	Thr 10 cac His aag Lys tgg Trp cgc Arg	aag Lys ctg Leu ccc Pro tac Tyr 75	ttc Phe acc Thr acc Thr 60 ccc Pro	val agc ser ctg Leu 45 ctc Leu gac Asp	Pro gtg Val 30 aag Lys gtg Val cac His	Ile 15 tcc Ser ttc Phe acc Thr atg Met	ggc Gly atc Ile acc Thr aag Lys 80 gag	:	96 144 192